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ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	BI829760 603079831	AA436088 zu03a08.r			AA435988 zu03a08.s	AA758635 ah67b04.s	AA470059 zt94h05.r	BE107659 UI-R-BT1-	U			AQ108532 CIT-HSP-2	AA707529 ah41a12.s	BF319786 uv63h11.x	BE638317 EST00003	BE638325 EST00022	BM253528 514627 MA
SUMMARIES	αī	BI829760	AA436088	A1149899	AA416972	AA435988	AA758635	AA470059	BE107659	AI002083	AA411806	AA781801	AQ108532	AA707529	BF319786	BE638317	BE638325	BM253528
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	uery Match Length DB	713	516	208	387	382	394	415	484	482	410	389	538	281	332	601	224	568
аÞ	Query	93.1	66.4	66.2	50.3	49.6	42.8	39.5	38.8	35.7	35.2	32.3	19.5	19.1	19.0	17.8	16.4	12.5
	Score	707.2	504.8	503.2	382.2	377.2	325.4	300.4	295.2	271	267.4	245.4	148.4	145	144.2	135	124.6	95
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RESULT 1 B1829760 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL COMMENT FEATURES SOURCE SOURCE	B1829760 713 bp mRNA linear EST 04-OCT-2001 603079831F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5171526 5', mRNA sequence. B1829760 B1829760 G1:15941310 EST. human.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 713) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) (Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Fissue Propurement: Life machonomics Inc	CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11426 row: n column: 07 High quality sequence stop: 713. High quality sequence stop: 713.	
	RESULT 1 B1829760 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES	source

us-09-821-821-1.rst

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Matches 506;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. this is a NIH_MGC Library. In 154 c 123 g 233 t 1 others
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (info@lmage.llnl.gov) for further information.
INAGE Length: 733 God Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 482.
Location/Qualifiers
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Pred. No. 1.7e-61;
); Mismatches 2;
                                                                                                                                                      Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:730742"
/clone_lib="Soares_testis_NHT"
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/organism="Homo sapiens"
/db_xref="GDB:5927437"
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Contact: Wilson RK
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/clone="IMAGE:730041"
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGPP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIAN at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 742 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. " 91 c 89 g 142 t
                                                                                                                                                           9643h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752827 3' similar to SW:CD20_HUMAN P11836 B-LYMPHOCYTE ANTIGEN CD20; Al149899
                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
Ph.D.
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/b_xref="taxon:9606"
/clone="IMAGE:1752827"
/clone_lib="Soares_testis_NHT"
                                                                                 aactacatttgtggttattctcaccaaa 554
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/note="Vector: pr7#3D-pac (Pharmacia) with a modified polylinker; Site_1: Not I: Site_2: Eco Rr; lst strand cDNA was prepared from mRNA obtained from Clontech Laboratories Inc., and primed with a Not I - oligo(dI) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA416972

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 387)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 649
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                                                                                                                            388 TCAGGATATCCATTCTGGGGCTCTGTTTTGTTCATTAATTCTGGAGCCTTCCTAATTGCA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 TCAATTTTGGGGTGCCACTCAGAGGATTGTGATTGTGAACAATGTTGTTGACTAGCACTG 29
350 tcaggatatccattctggggctctgttttgttcattaattctggagccttcctaattgca
                                                                                                                                                                                                                                                                                                                              gocotgggagoaatagotggaatoattotoctoacatttggtttcatootagatcaaaao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      590 ggaattttgattacattgatgactttcagcattattgaattattcatttctctgcctttc
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/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="GDB:5926570"
/db_xref="taxon:9606"
```

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AA758635 394 bp mRNA linear EST 29-DEC-1998 ah67b04.sl Soares_testis_NHT Homo sapiens CDNA clone 1320655 3' similar to SW:CD20_HUMAN P11836 B-LYMPHOCYTE ANTIGEN CD20 ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTGGTTATTCTCACCAAAATAGTCAGTGTAAGGCTGTTACTGTCCTGTTCTTGGGAATT 143
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Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Eutheria; Primates; Catarrhini; Hon
1 (bases 1 to 394)
NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                               Score 377.2; DB 9;
Pred. No. 1.2e-43;
0; Mismatches 3;
                                            1. 382
/organism-"Homo sapiens"
/db_xref="GDB:5917437"
/db_xref="taxon:9606"
/clone="IMAGE:730742"
/clone="lib="Soares_testis_NHT"
Seg primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 280.
Location/Qualifiers
                                                                                                                                                             /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             taaagatgtgttaaaatctcaa 737
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ilarity 99.2%;
Conservative
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Matches 379, Conserv
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38 similar to SW:CD20_HUMAN P11836 B-LYMPHOCYTE ANTIGEN CD20 ;,
AA435988
AA435988.1 GI:2140902
EST.
               Double-stranded CNNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and Cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo saplens
Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 382)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylle,T., Waterston,R. and Wilson,R.
   rgrtaccaarcrgaagrgggagggggcgcccaartrtrtrtrtrtrtr 3'].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Insert Length: 733 Std Brror: 0.00
                                                                                                                                                                                                                                                                                                                                                    585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Bdx 8501, St. Louis, MO 63108
Fax: 314 286 1810
                                                                                                                                                               Length 387;
                                                                                                                                                                                              Indels
                                                                                                                                                           Score 382.2; DB 9;
Pred. No. 2.4e-44;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         732
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Best Local Similarity 99.28;
Matches 384; Conservative
                                                                                               138
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SOURCE
ORGANISM
                                                                                              BASE COUNT
ORIGIN
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JOURNAL
COMMENT
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VERSION
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                  226
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Gaps

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Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108
4444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108
Fax: 314 286 1800
Fax: 314 286 1810
Email: est@watison.wustl.edu
This clone is available royalty-free through Lini.; contact the
IMAGE Consortium (infe@image.lini.gov) for further information.
Insert Length: 656 Std Error: 0.00
Seq primer: -28mil rav2 ET from Amersham
High quality sequence stop: 393.
Location/Qualifiers
                                                                                                                                  Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, White, Y., Wylie, T., Wylie, T., Waterston, R. and Wilson, R., Theising, B., Washu, W. I., Wylie, T., Waterston, R. and Wilson, R.
zt94h05.rl Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730041
5' similar to SW:CD20_HUMAN P11836 B-LYMPHOCYTE ANTIGEN CD20 ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gtetagaetgaagtaccaactaaatcateteettteaaattateaccgacaccateatgg 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 attcaagcaccgcacacagtccggtgtttctggtatttcctccagaaatcactgcttcag 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 aatatgagtccacagaactttcagccacgacctttcaactcaaagcccttgcaaaaat 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tatttgctagaaaaatgaaaatcttagggactatccagatcctgtttggaattatgacct 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GACTAGACTGAAGTACCAACTAAATCATCTCCTTTCAAATTATCACCGACACCATCATGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.5%; Score 300.4; DB 9; Length 415; 79.9%; Pred. No. 5.5e-33; ive 0; Mismatches 1; Indels 103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares_testis_NHT"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .415
/organism="Homo sapiens"
/db_xref="GDB:5926570"
/db_xref="taxon:9606"
/clone="IMAGE:730041"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 TATTTGCTAGAAAATGAAAATCTTAGG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
                                                                  AA470059.1 GI:2197368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 414; Conservative
                                   mRNA sequence.
                                                                                                                      Homo sapiens
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                                                                                                         human.
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/lmage/image.html
Insert Length: 661 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 390.

Location/Qualifiers
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                                                                                     M. Fatima Bonaldo
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tagtgccctgggagcaatagctggaatcattctcctcacatttg-gtttcatcctagatc 524
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                  Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D.,
Ph.D.
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                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="1320655"
/clone_lib="Soares_testis_NHT"
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/lab_host="DH10B"
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482 bp mRNA linear EST 27-AUG-1998 3', mRNA sequence.
AI002083 GI:3202120
EST. 27-AUG-1998
AI002083.1 GI:3202120
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nlh.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMM Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases i to 482)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                              558 gtcagtgtaaggctgttactgtcctgttcttgggaattttgattacattgatgactttca 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 TTCAGTGTGGTGCTATTACCACTCTATTTGTTGGTTTTTGATTATGTTGATCATCATCA 125
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                                                                                                                                                                                                                                                     318 aaccatatccaaggtttccctttatatttctttcaggatatccattctggggctctgttt 377
                                                                                                                                                                                                                                                                                                                   tgttcattaattctggagccttcctaattgcagtgaaaagaaaaccacagaaactctga 437
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9
                                                                                                                             Length 484;
                                                                                                                          Query Match 38.8%; Score 295.2; DB 9; Length Best Local Similarity 76.7%; Pred. No. 2.7e-32; Matches 376; Conservative 0; Mismatches 108; Indels
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6:791-806, 1996)
TAG_LIB=UI-R-BT1
TAG_TISSUE=testis
TAG_SEQ=AGGCAG"
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DE107659
BE107659.1 GI:8499769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: msoares@blue.weeg.ulowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNN and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NoII site
and the oligo-dT track served to identify it as a clone from the
normalized testis library cDNA tibrary Preparation: M.B. Soares Lab
Clone distribution: clones will be available through Research
Seq primer: Mi3 Forward
POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordața; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentța; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 484)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                401
                                                                                                                                                          ttottagtgccctgggagcaatagctggaatcattctcctcacatttggtttcatcctag 521
                                                                                                                                                                           451 Ecketein Medical Research Building Iowa City, IA 52242, Tel: 319 335 8250
Fax: 319 335 9565
                                342 tatttctttcaggatatccattctggggctctgttttgttcattaattctggagccttcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                   Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                          Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          discovery
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BE107659/c
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                                                             209
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TITLE
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COMMENT

FEATURES

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; ...

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

It (bases 1 to 410)

Stallier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,

Rucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,

Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.

Unpublished (1997)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA411806
zt67a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727372
3' similar to SW:CD20_HUMAN P11836 B-LYMPHOCYTE ANTIGEN CD20 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 608 Std Error: 0.00
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 401.
Location/Qualifiers
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70 ACTCAGAGGATTGTGATTGTGAACAATGTTGTTGACTAGCACTGTGAGAATAAAGATGTG 11
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Pred. No. 2.2e-28;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. 410
/organism="Homo sapiens"
/db_xref="GDB:594284"
/db_xref="taxon:9606"
/clone="IMAGE:727372"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="male"
/lab_host="DH10B"
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ilarity 96.1%;
Conservative
                                                                                                                                                                                 mRNA sequence.
AA411806
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Matches 274;
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AA411806/c
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cagaaactctgataatattgagccgaataatgaattttcttagtgccctgggagcaatag 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ccacgaccttttcaactcaaagcccttgcaaaaattatttgctagaaaaatgaaaatct 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GATCAAAACTACATTTTT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tagggactatccagatcctgtttggaattatgaccttttctttttggagttatcttccttt 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAGG----- 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----- 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tcatctctttcaattatcaccgacaccatcatggattcaagcaccgcacacagtccgg 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            482 TCATCTCCTTTCAAATTATCACCGACACCATCATGGATTCAAGCACCGCACACAGTCCGG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            486 ctggaatcattctcctcacatttggtttcatcctagatcaaaactacatttgtggttatt
                                                                                                                                                                                                                                                                                                                                                                                                  Score 271; DB 9; Length 482;
Pred. No. 6.3e-29;
0; Mismatches 0; Indels 188;
          found through the I.M.A.G.E. Consortium/LLNL at:
                     www-bio.llnl.gov/Dbrp/image/image.html
Insert Length: 598 Std Error: 0.00
Seq primer: -40ml3 Fwd. ET from Amersham
High quality sequence stop: 393.
                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9006"
/clone="IMAGE:1619019"
/clone_lib="Soares_testis_NHT"
                                                                                Location/Qualifiers
                                                                                                                                                                                  /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 71.8%;
Matches 479; Conservative
                                                                                                                                                                    /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 CAGAAACTCT-
                                                                                                                                                                                                                                                                                                                                                 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215
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AQ108532 53-AUG-1998
CIT-HSP-2379G7.TF CIT-HSP Homo sapiens genomic clone 2379G7, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter, J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
Unpublished (1998)
Other_GSSs: CIT-HSP-2379G7.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Email: mdadamsetigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia: Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 538)

Adams, M.D., Rounaley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,

Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: MI3-21
Class: BAC ends.
631 attoatttototgootttotoaattttggggtgooactoagaggattgtgattgtgaaca 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               571 tgttactgttcctgttcttgggaattttgattacattgatgactttcagcattattgaatt 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                          269 CCATATCCAAGGTTTCCCTTTATATTTCTTTCAGGATATCCATTCTGGGGCTCTGTTTTG
                                                                                                                                              380 ttcattaattctggagccttcctaattgcagtgaaaagaaaaaccacagaaactctgata
                                                                       320 ccatatccaaggtttccctttatatttctttcaggatatccattctggggctctgtttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 19.5%; Score 148.4; DB 12; Length Best Local Similarity 93.4%; Pred. No. 6.8e-12; Matches 155; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="CIT-HSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 g
                                                                                                                                                                                                                   440 atattgagccgaataatgaattt 462
                                                                                                                                                                                                                                                   149 ATTTTGATTACATTGATGACTTT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="2379G7
                                                                                                                                                                                                                                                                                                                                                                                                                   AQ108532.1 GI:3485222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex-"Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 c
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AQ108532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M. Fatima Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing Center
Information can be
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 389)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357
                                                                       417
                                                                                          Gaps
 358 tecattetggggetetgtttgtteattaattetggageetteetaattgeagtgaaaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Emal: cgapbs remail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coma Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sclone distribution: NCI-CGAP Colone distribution found through the I.M.A.G.E. Consortium/LiNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 983 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                            418 aaaaaccacagaaactctgataatattgagccgaataatgaattt 462
                                                                                                                                                               170 AAAAACCACAGAAACTCTGGGGAATTTTGATTACATTGATGACTTT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 245.4; DB 9;
Pred. No. 2.6e-25;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .389
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="1375056"
/clone=lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                            sequence.
AA781801
AA781801.1 GI:2841132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex-"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 252; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140
                                                                                                                                                                                                                                                                                                                                                                                                  human.
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LOCUS
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AUTHORS
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 298
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COMMENT
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KEYWORDS
SOURCE
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Gaps

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8

Length 538;

us-09-821-821-1.rst

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/ssve_type="round spermatids, pooled from multiple mice"
/dsv_atage="60 day"
/lab_host="bH10B (phage=resistant)"
/note="Organ: testis; Vector: pBluescript SK+ (Stratagene)
/note="Organ: testis; Vector: pBluescript SK+ (Stratagene); Site_1: XhoII; Site_2: EcoRI; cDNA oligo dT-primed
[5'-(GA)IO-ACTAGTCTGAGTTTTTTTTTTTTTT-7:] and directionally
cloned using 5' linkers 5'-AATTGGGAGGAG-3' and
5'-CTGGTGCG-3'. Size selection of >400bp material gives
average insert size ranging from 1-2 kb. Library was mass
excised (from lambda-UniAAP-XR) and resulting
single-stranded phagemids were prepped and tranformed
into DH10B. Library contains 98:3% recombinants.
References: J. Androl. 20:635-639 and Gene 23:263-269.
Library constructed and donated by J. McCarrey, Ph.D.
(Southwest Poundation for Biomedical Research, Dept. of
Genetics); excision done by E.M. Eddy, Ph.D. (National
Health Sciences). Original lambda-based library is
available through ATCC, catalog #63423:"
                                                                                                                                                                                                                                                                   Mus musculus

Butaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Hammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

E 1 (bases 1 to 332)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylle,T.,

Underwood,K., Steptoe,M., Thelsing,B., Allen,M., Bowers,I., Person

B., Swaller,T., Gibbon,M., Pape,D., Harvey,N., Schurk,R.,

E, Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,

The Washlorn R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999

Unpublished (1999)

Washington University School of Medicine

4444 Prozets Park Parkway, Box 8501, St. Louis, MO 63108, USA

Fax: 314 286 1810
                                                                                                o mRNA linear EST 29-DEC-2000 spermatid Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1425061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          439 aatattgagccgaataatgaattttcttagtgccctgggagcaatagctggaatcattct 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     379 gttcattaattctggagccttcctaattgcagtgaaaagaaaaccacagaaactctgat 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.0%; Score 144.2; DB 10; Length 332; 76.9%; Pred. No. 3.5e-11; Live 0; Mismatches 53; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="TMAGE:3664293"
/clone="IMAGE:3664293"
/sex="male"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .332
/organism="Mus musculus"
/strain="CD-1"
                                                                                          332 bp
uy63hll.xl McCarrey Eddy round sp
IMAGE:3664293 3', mRNA sequence.
BF319786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 313.
Location/Qualifiers
                                                                                                                                                                                                BF319786.1 GI:11268601
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                                                                                                                                                                                                                                                       house mouse.
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Best Local Simi:
Matches 176; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGPP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 456 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                         bp mRNA linear EST 12-JAN-1999
Homo sapiens cDNA clone 1292062 3',
                                                                                                                                                                                                                                                                                                                                                                                                 Homo saplens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Butheria; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 281)

NOI-GEAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)
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Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 145; Conservative 0; Mismatches 0; Indels
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                                                                          1. .281
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                                                                                                                                                                                                                                                                              mRNA sequence.
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EST00003 mouse testis apoptosis subtraction cDNA library Mus musculus cDNA clone MTA03 5', mRNA sequence.

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Mus musculus

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 601)

Jiang, H., Li,L. and Lu,G.

Expressed sequence tags from mouse testis apoptosis subtraction

CONA library
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Contact: Jiang H
Contact: Jiang H
Department of Pharmacology
Hunan Medical University
Hunan Medical University
8 Xiangya road, Changsha, Hunan 410078, China
Tel: 086-0731-4497661
Fax: 086-0731-4497661
Email: 1j12@public.cs.hn.cn
Seq primer: T7 Promoter Primer
High quality sequence stop: 601.
Coation/Qualifiers

/ Strain="C57BL"
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/ Clone="Musculus"
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August 27, 2002, 11:02:16; Search time 26.58 Seconds (without alignments) 1301.692 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                OM protein - protein search, using sw model
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Perfect score:
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Maximum DB seq
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

sp_fungi:* sp_human:* sp_invertebrate:*

sp_mammal:*

sp_archea:*
sp_bacteria:*

SPTREMBL_19:*

Database :

sp_unclassified:* sp_vertebrate:* sp_rv1rus:* sp_bacteriap:* sp_organelle:* sp_phage:* sp_plant:* sp_rodent:* sp_archeap:* sp_virus:* sp_mhc:* 5: 6: 7: 111: 112: 114: 116:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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df	Query	100.0	99.4	19.7	19.7	19.7	19.5	18.4	18.3	18.1	17.9	17.9	17.8	17.5	17.4	17.1	16.9
	Score	1027	1021	202.5	202.5	202.5	200.5	188.5	187.5	185.5	183.5	183.5	182.5	180	178.5	176	174
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1 MDSSTAHSPVFLVFPPEITASEYESTELSATTFSTQSPLQKLFARKMKILGTIQILFGIM 60

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16.8 220 11 16.8 267 4 0 16.7 178 4 0 16.7 679 4 0 16.4 249 4 0	167 16.3 268 11 095020 165 16.1 135 6 095174 160.5 15.6 213 11 092004 160.5 15.6 240 4 0962W8 158.5 15.4 247 11 099N07	5.5 15.1 247 11.5 15.0 244 11.6 11.5 14.2 250 4	13.6 190 11 13.4 124 11 13.4 167 4 13.4 230 11 13.2 234 11	123 12.0 125 11 0912Y5 108.5 10.6 215 11 09D2W6 106 10.3 307 16 09CES9 103 10.0 175 11 09D7R4 103 10.0 455 5 019442 100 9.7 152 4 014298 96 9.3 387 16 09PN01 95.5 9.3 355 17 096ZJ3
17 18 19 20 21	22 23 24 25 26	30 30 31 32	33 35 37 37	8 6 0 H G E E E E

ALIGNMENTS

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MEDLINE=21295030; PubMed=11401424;
Liang Y., Tedder T.F.;
"Identification of a CD20-, FcepsilonRibeta-, and HTm4-Related Gene Family: Sixteen New MS4A Family Members Expressed in Human and Mouse.";
                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Sablbashi K., Sasaki S., Marumo F.;
"Cloning of three CD20 homolog from human, putative calcium
channels.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                     Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                     Genomics 72:119-127(2001).
EMBL; AB013103; BAB18739.1; -.
EMBL; AF237907; AAK37416.1; -.
SEQUENCE 200 AA; 22283 MW; F9282E5D15BC5514 CRC64;
                                                                         Last sequence update)
Last annotation update)
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SEQUENCE FROM N.A.
                             Q9H3V2
RESULT
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98 SGAFLIAVKRKTTETLIILSRIMNFLSALGAIAGIILLTF--GFILDQNYICGYSHQNSQ 155
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       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                            SEQUENCE FROM N.A.
MEDLINE-21142397; Pubmed-11245982;
Ishibashi K., Suzuki M., Sasaki S., Imai M.;
"Identification of a new multigene four-transmembrane family (MS related to CD20, HTm4 and beta subunit of the high-affinity IgE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-PLACENTA;
MEDLINE-21255030; PubMed-11401424;
Liang Y., Tedder T.F.;
Tidentification of a cd20-, feepsilonribeta-, and htm4-related
family: sixteen new ms4a family members expressed in human and
mouse.";
                                                                                                                                                            FEAC...;

Gene 264:87-93(2001).

GNBL; AB013102; BAB18738.1; -.

EMBL; AB013102; BAB18738.1; -.

EMBL; AB013102; BAB18738.1; -.
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EMBL; AF237912; AAK37594.1; -.
SEQUENCE 220 AA; 23220 MW; 7648C762197C1179 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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; Pred. No. 1.2e-10;
31; Mismatches 71;
                                                                                                                                                                                                                                                                                19.7%; Score 202.5; DB 4
31.8%; Pred. No. 1.1e-10;
tive 31; Mismatches 71
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31.8%;
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Best Local Similarity
Matches 49; Conserv
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Best Local Similarity
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                                                         NFLSALGAIAGIILLTFGFILDQNYICGYSHQNSQCKAVTVLFLGILITLMTFSIIELFI 180
                                                                                                                               NFLSALGAIAGIILLTFGFILDQNYICGYSHQNSQCKAVTVLFLGILITLMTFSIIELFI 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21092614; PubMed=11162526; Hogarth P.M., Eyre H.J., Hulett M.D., Pagler E., Hornby J.R., Hogarth P.M., Eyre H.J., Hulett M.D., Pagler E., authorland G.R., Ohms S.J., Parish C.R., Isolation, tissue distribution, and chromosomal localization of a novel testies specific human four transmembrane gene related to CD20 Biochem. Blophys. Res. Commun. 280:374-379(2001).
MDSSTAHSPVFLVFPPEITASEYESTELSATTFSTQSPLQKLFARKMKILGTIQILFGIM
                                      TFSFGVIFLFTLLKPYPRFPFIFLSGYPFWGSVLFINSGAFLIAVKRKTTETLIILSRIM
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Pred. No. 4.3e-84;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TESTIS-EXPRESSED TRANSMEMBRANE-4 PROTEIN.
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Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last anno
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Best Local Similarity 99.5%;
Matches 199; Conservative (
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(TrEMBLrel. 16, I
(TrEMBLrel. 19, I
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01-MAR-2001
01-DEC-2001
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Length 220; Indels

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Rawai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y., A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., A Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Astor T., Okazaki Y., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Redischmann W., Gasterland T., Gissi C., King B., Kochiwa H., Redischmann W., Gasterland T., Gissi C., King B., Kochiwa H., Schriml L.M., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T., Barak K., Okido T., Furuki R., Tomita M., Gariboldi M., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Flefcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Asaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F., Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Mashizaki Y., Rawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 RIMNFLSALGAIAGIILLTFGFI-------LDQNYICG-YSHQNSQCKAV 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 FSFGVIFLFTLLKPYPRFPFIF----LSGYPFWGSVLFINSGAFLIAVKRKTTETLIILS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_raxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 DSSTAHSPVFLVFPPEITASEYESTELSATTFSTQSPLQKLFARKMKILGTIQILFGIMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 11; Length 217;
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SEQUENCE 217 AA; 23643 MW; ZE6C4FF0287B543F CRC64;
                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
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26.4%; Pred. No. 2.1e-09;
tive 40; Mismatches 80
                                                                                                                                                                                                                    217 AA.
                                                                                                        132 CHGTMSILMGLDGMVLLLSVLEFCIAVSLSAFGC 165
                                                               156 CKAVTVLFLGILITIMIFSIIELFISLPFSILGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-C57BL/6J; TISSUE-STOMACH;
MEDLINE-21085660; PubMed=11217851;
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17,
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EMBL; AK008652; BAB25808.1;
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2200009H22RIK PROTEIN.
2200009H22RIK.
                                                                                                                                                                                                                                                                                      (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
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Best Local Similarity
Matches 55; Conserv
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 SGAFLIAVKRKTTETLIILSRIMNFLSALGAIAGIILLTF--GFILDQNYICGYSHQNSQ 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 LQKLFAR-KMKILGTIQILFGIMTFSFGVIFLFTLLKPYPRFPFIFLSGYPFWGSVLFIN 97
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                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                 Full Y., Takayama K.; "Characterization of a Fc epsilon receptor beta subunit homolog lacking ITAM motif."; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB022821; BAB61018.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 19.7%; Score 202.5; DB 4; Length 239; Best Local Similarity 31.8%; Pred. No. 1.3e-10; Matches 49; Conservative 31; Mismatches 71; Indels 3.
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                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MRNA SIMILAR TO FC EPSILON RECEPTOR BETA SUBUNIT, COMPLETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhao Z., Huang X., Li N., Zhu X., Cao X.;
"A novel gene from human dendritic cell.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF068288; AARF65507.1;
SEQUENCE 197 AA; 20909 MW; 11F056CA869616A7 CRC64;
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Last annotation update)
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                                                               239 AA
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nes 49; Conserva
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                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. TISSUE-BLOOD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                             096705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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Matches
                  RESULT
096JQ5
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60 MTFSFGVIFLFTLLKPY----PRFPFIFLSGYPFWGSVLFINSGAFLIAVKRKTTETLII 115
                                   116 LSRIMNFLSALGAIAGIILLTFGFILDQNYI--CGYSHQNSQ----CKAVTVLFLGILIT 169
                                                                                                                                 120 NSFGMNIASATIALVGTAFLSLNIAVNIQSLRSC--HSSSESPDLCNYMGSISNGWYSL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liang Y., Buckley T.R., Tu L., Langdon S.D., Tedder T.F.;
"Structural organization of the human MS4A gene cluster on Chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 VLSLGIILASASFSPNFTQVTSTLLNSAYPFIGPFFFIISGSLSIATEKRLTKLLVHSSL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TFSFGVIFLFTLLKP-YPRFPFIFL-SGYPFWGSVLFINSGAFLIAVKRKTTETLIILSR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 IMNFLSALGAIAGIILL-----TFGFILDQN----YICGYSHQN---SQCKAV 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MDSSTAHSPVFLVFPPEITASEYESTELSATTFSTQSPLQKLFARKMKILGTIQILFGIM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MTSQPVPNETIIVLPSNVI--NFSQAEKPEPTNQGQDSLKKHLHAEIKVIGTIQILCGMM 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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EMBL; AF354930; AALO7357.1; -
SEQUENCE 225 AA; 24331 MW; 12FBF5DCDC71B56A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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01-MAR-2001 (TrEWBLrel. 16, Last sequence update)
01-DEC-2001 (TrEWBLrel. 19, Last annotation update)
CDA01 (MS4A6A-POLYMORPH) (MS4A6A PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 17.9%; Score 183.5; DB 4; Best Local Similarity 26.4%; Pred. No. 6e-09; Matches 55; Conservative 39; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                           225 AA
                                                                                                                                                                                                                               170 LMTFSIIELFISLPFSILGCHSEDCDCEQ 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 TVLFLGILITLMTFSIIELFISLPFSIL 187
                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21382044; PubMed-11486273;
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                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
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SEQUENCE FROM N.A.
TISSUE=PHEOCHROMOCYTOMA;
                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSFGVIFLFTLLKPYPRFPFIF----LSGYPFWGSVLFINSGAFLIAVKRKTTETLIILS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----ILDQNYICG-YSHQNSQCKAV 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 LTLNILSVSFAFVGIIIISVSLAGLHPASEQCKQSKELSLIEHDYYQPFYNSDRSECAVT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 DSSTAHSPVFLVFPPEITASEYESTELSATTFSTQSPLQKLFARKMKILGTIQILFGIMT 61
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                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Cațarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                      htm4-related
in human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 18.3%; Score 187.5; DB 11; Length 217; Best Local Similarity 26.0%; Pred. No. 2.5e-09; Matches 54; Conservative 41; Mismatches 80; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 18.1%; Score 185.5; DB 4; Length 214; Best Local Similarity 28.7%; Pred. No. 3.8e-09; Matches 60; Conservative 39; Mismatches 85; Indels 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Straubberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC008487; AAH08487.1; -.
SEQUENCE 214 AA; 22933 MW; D30C276213DB8F3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: AF237910; AAK37419.1; -.
SEGUENCE 217 AA; 23622 MW; 8BF521AF22DBB7BD CRC64;
                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MS4A6C PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last isequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:14809).
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUB-TOTAL FETUS.
TISSUB-TOTAL FETUS.
Lidang Y., Tedder T.F.;
"Identification of a cd20-, fcepsilonribeta-, and family: sixteen new ms4a family members expressed
  217 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 TVLFLGILITLMTFSIIELFISLPFSIL 187
  PRT;
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  PRELIMINARY;
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TISSUE-LUNG CARCINOMA;
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                                                                                                                                                                                                                       NCBI_TaxID=10090;
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90
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liang Y., Tedder T.F.; "Identification of a CD20-, FcepsilonRIbeta-, and HTm4-Related Family: Sixteen New MS4A Family Members Expressed in Human and Mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Venkataraman C., Schaefer G., Schindler U.; "Chandra, a novel four transmembrane protein differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in helper type I lymphocytes."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
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EMBL; AF230640; AAG09739.1; -.

EMBL; AF237913; AAK37555.1; -.

MMGD; MGI: 1913083; L9116.

SEQUENCE: 226 AA; 24090 MW; 78C6ED3E830AA116 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 SQCKAVTVLFLGILITIATFSIIELFISLPFSILGCHSEDCDCEQ 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                         01-WAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CHANDRA PROTEIN (MS4A4B PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.5%; Score 180; DB 11; 26.1%; Pred. No. 1.2e-08; iive 36; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ä.
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                                                                                                                179 KASLAGSLSLMLICTLLEFCLAVLTAVL 206
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MEDLINE=21295030; PubMed=11401424;
                                                                             160 TVLFLGILITLMTFSIIELFISLPFSIL
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01-DEC-2001 (TrEMBLrel. 19,
MS4A4D PROTEIN.
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Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                        Q9ES61;
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                                                                                                                                                                                                                     RESULT 13
Q9ES61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 IMNFLSALGAIAGIILL-----TFGFILDQN----YICGYSHQN---SQCKAV 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TFSFGVIFLFTLLKP-YPRFPFIFL-SGYPFWGSVLFINSGAFLIAVKRKTTETLIILSR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TFSFGVIFLFTLLKP-YPRFPFIFL-SGYPFWGSVLFINSGAFLIAVKRKTTETLIILSR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 IMNFLSALGAIAGIILL-----TFGFILDQN-----YICGYSHQN---SQCKAV 159
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                          SEQUENCE FROM N.A.
TISSUE-LIVER, AND SPLEEN;
MEDLINE-21295030; PubMed-11401424;
Liang Y., Tedder T.F.;
"Identification of a CD20-, FoepsilonRibeta-, and HTM4-Related (Femily: Sixteen New MS4A Family Members Expressed in Human and Mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
     Chen
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"Novel human CD20-11ke molecule.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF142409; AAG27920.1; -.
                                                      Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                               EMBL; AF212240; AAG41780.1; -
EMBL; AF212240; AAK3794.1; -
EMBL; AF219908; AAK3794.1; -
EMBL; AF237908; AAK3747.1; -
SEQUENCE 248 AA; 26943 MW; 49892BC25D220A23 CRC64;
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     Q., Peng, y, Song H., Yu Y., Xu S., Ren
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.9%; Score 183.5; DB 4; 26.4%; Pred. No. 6.6e-09; tive 39; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 AA
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Best Local Similarity
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        Y., Huang
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                                                                                                                                                                                                                                                                     Query Match 17.4%; Score 178.5; DB 11; Length 225; Best Local Similarity 31.4%; Pred. No. 1.7e-08; Matches 50; Conservative 35; Mismatches 61; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 SGAFLIAVKRKTTETLILLSRI-MNFLSÅLGAIAGIILLTFGFILDQNYICGY---SHQN 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 QKLFARKMKILGTIQILFGIMTFSFGVİFLFTLLKPYPRFPFIFLSGYPFWGSVLFINSG 99
                                                                                                                                                                                                                     34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MDSSTAHSP----VFLVFPPEI------TASE---YESTELSATTFS-----TQS 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 PLOKLFARKMKILGTIQILFGIMTFSFGVIFLFTLLKPYPRFPFIFLSGYPFWGSVLFIN 97
                                      Liang Y., Tedder T.F.; Tedder T.F.; Tedentification of a cd20-, fcepsilonribeta-, and htm4-related gene family: sixteen new ms4a family members expressed in human and mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 27.1%; Score 176; DB 11; Length 268;
Best Local Similarity 27.1%; Pred. No. 3.3e-08;
Matches 60; Conservative 36; Mismatches 91; Indels 3
                                                                                                                9D3B2678787039B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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145 A--SLDVLATIL--NMLEFCIAVSVSAFGCKASCCNSSE 179
                                                                                                                                                                                                                                                                                                                                                                                               268 AA.
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                       MEDLINE-21295030; PubMed-11401424;
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Search completed: August 27, 2002, 11:05:06 Job time: 170 sec

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SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
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TOPOLOGY: linear
MMEDIATE SOURCE:
LIBRARY: BRAINOTO4
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2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/pcTuS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-994-578-4
US-09-213-389-3
US-07-869-933-29
US-07-869-933-33
US-08-201-879A-4
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US-09-103-663-29
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S-09-103-663-23
S-07-869-933-34
S-08-201-879A-5
S-09-103-663-34
S-07-869-933-35
S-08-201-879A-3
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Maximum DB
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60 MTFSFGVIFLFTLLKPY----PRFPFIFLSGYPFWGSVLFINSGAFLIAVKRKTTETLII 115
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   54 LQEKFLKGEPKVLGVVQILTALMSLSMGITMMCMASNTYGSNPISVYIGYTIWGSVMFII 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 LSRIMNFLSALGAIAGIILLTFGFILDQNYI--CGYSHQNSQ----CKAVTVLFLGILIT 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 25;
                                                                                                                                                                                                                                   Sequence 4, Application US/08318492
Fatent No. 5552312
GENERAL INFORMATION:
APPLICANT: Lim, Bing
APPLICANT: Lelias, Jean-Michel
TITLE OF INVENTION: RECOMBINANT HTM4 GENE, PROTEIN AND
TITLE OF INVENTION: ASSAYS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMAILTON, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TIM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,492
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28.2%; Pred. No. 5.2e-13;
tive 38; Mismatches 87
                                                                                                                156 CKAVTVLFLGILITLMTFSIIELFISLPFSILGC 189
                                                                                                                                     170 LMTFSIIELFISLPFSILGCHSEDCDCEQ 198
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CLASSIFTCATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: BROOK, DAVID E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: BIH94
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 861-6240
INFORMATION FOR SEC ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 214 amino acids
amino acid
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Best Local Similarity
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US-08-318-492-4
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                                       Gaps
                                                                          39 LQKLFAR-KMKILGTIQILFGIMTFSF¢VIFLFTLLKPYPRFPFIFLSGYPFWGSVLFIN 97
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19.7%; Score 202.5; DB 2; Length 239; 31.8%; Pred. No. 2.4e-15; Live 31; Mismatches 71; Indels 3
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                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09213389
Fatent No. 5977072
GENERAL INFORMATION
FAPELICANT: Lal, Preeti
APPLICANT: Colley, Nell C.
TITLE OF INVENTION: HIGH AFFINITY IMMUNOCLOBULIN E
TITLE OF INVENTION: RECEPTOR-LIKE PROTEIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.4e-15;
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OPERATING SYSTEM: DOS
SOFTMARE: FASTSEC for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                        156 CKAVTVLFLGILITLMTFSIIELFISLPFSILGC 189
                                                                                                                                                                                                                                             174 CHGTMSILMGLDGMVLLLSVLEFCIAVŞLSAFGC 207
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19.7%; Score 202.5;
Best Local Similarity 31.8%; Pred. No. 2.4e
Matches 49; Conservative 31; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: B111ngs, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0371 US
TELECHMUNICATION INFORMATION:
TELEPHONE: 415-845-4166
TELEFAX: 415-845-4166
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APPLICATION NUMBER: 08/916,902
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IBM Compatible
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Query Match
Best Local Similarity 31.8%.
Matches 49; Conservative
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MEDIUM TYPE: Diskett
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CLONE: 927955
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STATE: CA
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US-09-213-389-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDSSTAH-SPVFLVFPPEITASEYESTELSATTFSTQSPLQKLFARKMKILGTIQILFGI 59
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                                                                     Sequence 4, Application US/08707340
Patent NO. 5705615
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL Lim, Bing
APPLICANT: Lain, Bing
APPLICANT: Lelias, Jean-Michel
TITLE OF INVENTION: RECOMBINANT HTM4 GENE, PROTEIN AND
MINDER OF SATTAMENTOR: ASSAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/707,340

FILING DATE: 03-SEP-1996

CLASSIFCATION NUMBER: US/08/707,340

FILING APPLICATION DATA:

APPLICATION NUMBER: US/08/318,492

FILING APPLICATION DATA:

APPLICATION NUMBER: US/08/55,648

FILING APPLICATION DATA:

APPLICATION NUMBER: US/08/55,648

FILING APPLICATION NUMBER: US/08/55,648

FILING APPLICATION NUMBER: US/08/55,648

FILING APPLICATION NUMBER: US/08/55,648

FILING APPLICATION NUMBER: US/08/55,648

TELECOMMUNICATION NUMBER: BIH94-03A2

REFERENCE/DOCKET NUMBER: BIH94-03A2

TELEPHONE: (617) 861-9540

INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                               E: Hamilton, Brook, Smith & Reynolds, P.C. Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.7%; Score 181.5; DB 1; 28.2%; Pred. No. 5.2e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 28.2%
Matches 59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-707-340-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                      JS-08-707-340-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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60 MTFSFGVIFLFTLLKPY----PRFPFIFLSGYPFWGSVLFINSGAFLIAVKRKTTETLII 115
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                                                                                                                                                                                            APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HIGH AFFINITY IMMUNOGLOBULIN E
TITLE OF INVENTION: RECEPTOR-LIKE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.7%; Score 181.5; DB 2; ilarity 28.2%; Pred. No. 5.2e-13; Conservative 38; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPATING SYSTEM: DOS
SOFTWARE: FastERO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,902A
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| ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::
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Sequence 3, Application US/08916902A
Patent No. 5871930
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 4, Application US/08994578
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: Herewith CLASSIFICATION: 536 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
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Matches 59; Conserv
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; CLONE: 561639
US-08-916-902A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: CA
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US-08-994-578-4
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Query Match
Best Local Similarity 28.29
Matches 59; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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CLONE: 561639
                                                                                                                                                                                                                                                                                                                                            Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDSSTAH-SPVFLVFPPEITASEYESTELSATTFSTQSPLQKLFARKMKILGTIQILFGI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 214;
                                                  APPLICANT: Lim, Bing
APPLICANT: Adra, Chaker N.
APPLICANT: Lellas, Jean-Michel
TITLE OF INVENTION: HTM4 METHODS OF TREATMENT AND ASSAYS,
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                          ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THE PC compatible
COMPUTER: THE PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/994,578
FILING DATE: December 19, 1997
CLLASSIFICATION: DATA:
APPLICATION NUMBER: US 08/707,340
FILING DATE: 03-SEP-1996
FILING DATE: US 08/707,340
FILING DATE: US 08/318,492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 17.7%; Score 181.5; DB 2; Best Local Similarity 28.2%; Pred. No. 5.2e-13; Matches 59; Conservative 38; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: B194-03A2Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEPHONE: (781) 861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
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; Sequence 3, Application US/09213389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 214 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-994-578-4
                                                                                                                                                                                                                                                                                                                                                                                                     U.S.A.
                               GENERAL INFORMATION:
Patent No. 5972688
                                                                                                                                                                                                                                                                                                                                                                                                                               02173
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116 LSRIMNFLSALGAIAGIILLTFGFILDQNYI--CGYSHQNSQ----CKAVTVLFLGILIT 169
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Baldman, Olga

APPLICANT: Lal, Preeti

TITLE OF INVENTION:

TITLE OF INVENTION: RECEPTOR-LIKE PROTEIN

NUMBER OF SEQUENCES: 4

CORRESPONDENCES: 4

CORRESPONDENCES: 1

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.7%; Score 181.5; DB 2; 28.2%; Pred. No. 5.2e-13; tive 38; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/213,389
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APPLICATION NUMBER: 08/916,902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
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GENERAL INFORMATION:

APPLICANT: KINET, Jean-Pierre

APPLICANT: KINET, Jean-Pierre

APPLICANT: KINET, Jean-Pierre

APPLICANT: JOUVIN, MAILE-Helene

APPLICANT: JOUNIN, MAILE-Helene

APPLICANT: JOUNIN, MAILE-HELENE

TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR 
TITLE OF INVENTION: IMMUNOGLOBULIN E

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSER: FOLLY & Lardner

STREET: JOUN K Street, N.W., Suite 500

CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 243;
                                       COMPUTER: READPRY disk
COMPUTER: FLOPPY disk
COMPUTER: IBM PC COMPAtible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPANIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,933
FILING DATE: 19920416
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFRENCE/CDCKET NUMBER: 40399/154 NIHD
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAS: (703)836-9300
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 24-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 15.4%; Score 158; DB 1, Best Local Similarity 28.0%; Pred. No. 3e-10; Matches 45; Conservative 28; Mismatches 7
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COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
TYPE: PLOPPY disk
MEDIUM TYPE: PLOPPY disk
TYPE: PLOPPY disk
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Patent No. 5807988
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INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
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                         COMPUTER READABLE FORM:
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US-08-201-879A-4
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Patent No. 5770396
GENERAL INFORMATION:
TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR TITLE OF INVENTION: IMMUNOGLOBULIN NUMBER OF SEQUENCES: 34 CORRESPONDENCE ADDRESS:
ADDRESSEE: Folse & Lardner STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                   TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR TITLE OF INVENTION: IMMUNGIOBULIN NUMBER OF SEQUENCES: 34
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Poley & Lardner STREET: 1800 Diagonal Road, Suite 500
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Best Local Similarity 28.0%; Pred. No. 3e-10;
Matches 45; Conservative 28; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                            COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,933
FILING DATE: 1992016
CLASSIFICATION: 514
ATTONREY/AGENT INFORMATION:
NAME: BENTY Stephen A.
REGISTRATION NUMBER: 29,768
REFRENCE/DOCKET: NUMBER: 29,768
REFRENCE/DOCKET: NUMBER: 29,768
TELEFRAX: (703)836-9300
TELEFRAX: (703)836-9300
TELEFRAX: (703)836-9300
TELEFRAX: (703)836-9300
TELEFRAX: GARACTERISTICS:
LENGTH: 243 mainto acids
TYPE: AMINO ACID
TOPPLOGY: linear
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KINET, Jean-Pierre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                            ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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                                                                                                                                                                                                                  CITY:
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   72; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                      15.4%; Score 158; DB 2; Length 243; 28.0%; Pred. No. 3e-10; tive 28; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMUNOGLOBULIN E
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Sequence 4, Application US/09213389

Sequence 597070:

Batent No. 597700:

APPLICANT: Bandman, Olga

APPLICANT: Lal, Preeti

APPLICANT: Lal, Preeti

TITLE OF INVENTION: RECEPTOR-LIKE PROTEIN

NUMBER OF SEQUENCES:

ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SUFTWARE: FastSEQ for Windows Version 2.0
SUSTEMIT APPLICATION DATA:
APPLICATION NUMBER: US/09/213,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERNCE/DOCKET NUMBER: PF-0371 US
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                      PF-0371 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/916,902
FILING DATE:
               REGISTRATION NUMBER: 36,749
                                    REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
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                                                                                                                                                                                    LENGTH: 243 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 28.0%
Matches 45; Conservative
                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415-845-4166
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; CLONE: 204117
US-08-916-902A-4
                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                     TOPOLOGY: 11ne
IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 15.4%; Score 158; DB 1; Length 243;
Best Local Similarity 28.0%; Pred. No. 3e-10;
Matches 45; Conservative 28; Mismatches 72; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 QSPLQKLFARKMKILGTIQILFGIMTFSFGVIFLFTLLKP--YPRFPFIFLSGYPFWGSV 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08916902A
Patent No. 5871930
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HIGH AFFINITY IMMUNOSLOBULIN E
TITLE OF INVENTION: RECEPTOR-LIKE PROTEIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 SQCKAVT-----VLFLGILITLMTFSITELFISLPFSIL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FESTERED FOR Windows Version 2.0
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,902A
FILING DATE: Herewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/869,933
FILING DATE: 16-APR-1992
PRIOR APPLICATION NUMBER: PCT/US93/03419
FILING DATE: 16-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/234/NIHD
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: USA
                                                                                                                                                                                                                                                              TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 243 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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US-08-201-879A-4
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REPERENCE/DOCKET NUMBER: 4039
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFACK: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 246 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 15.4%
Best Local Similarity 28.0%
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-103-663-33
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CLASSIFICATION:
  GENERAL INFORMATION
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US-07-869-933-23
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                                                                                                                                                                                                                                                             SEQ ID NO 33
LENGTH: 243
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Patent No. 6771803
GENERAL INFORMATION:
TATLE OF INVENTION: Isolation, characterization, and use of the human beta
TITLE OF INVENTION: Isolation, characterization, and use of the human beta
TITLE OF INVENTION: subunit of the high affinity receptor for
TITLE OF INVENTION: immunoglobulin E.
TITLE OF INVENTION: immunoglobulin E.
TITLE OF INVENTION: MUMBER: US/09/103,663D
CURRENT FILING DATE: 1998-06-23
EARLIER APPLICATION NUMBER: 07/869,933
EARLIER PILING DATE: 1992-04-16
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 29
LENGTH: 243
TITLE PATENTING DATE: 1998-06-26
SERVINEM: Homo sapiens
US-09-103-663-29
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tive 28; Mismatches 72;
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; Patent No. 6171803
                                        LENGTH: 243 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
INMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 204117
INFORMATION FOR SEQ 1D NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 28.09
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-09-103-663-33
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US-09-213-389-4
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Sequence 23, Application US/07869933

Sequence 23, Application US/07869933

Patent NO. 5770396

GENERAL INFORMATION:
APPLICANT: KINET, Jean-Pierre
TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR TITLE OF INVENTION: IMMUNOGLOBULIN NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                        and use of the human beta receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 QQTWQSFLKKELEFLGVTQVLVGLICLCFGTVVCSTLQTSDFDDEVLLLYRAGYPFWGAV 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 QSPLQKLFARKMKILGTIQILFGIMTFSFGVIFLFTLLKP--YPRFPFIFLSGYPFWGSV 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.4%; Score 158; DB 4; Length 243 28.0%; Pred. No. 3e-10; tive 28; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,933
FILING DATE: 19920416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 SQCKAVT-----VLFLGILITLMTFSIIELFISLPFSIL 187
APPLICANT: Kinet et al.
TITLE OF INVENTION: Isolation, characterization, and
TITLE OF INVENTION: subunit of the high affinity rec
TITLE OF INVENTION: immunoglobulin E.
FILE REFERENCE: 50490
CURRENT APPLICATION NUMBER: US/09/103,663D
CURRENT FILING DATE: 1998-06-23
FARLIER PILING DATE: 1998-06-43
FARLIER PILING DATE: 1998-06-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PATCHING DATE: 1908-06-23
NUMBER OF SEQ ID NOS: 35
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; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-869-933-23
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3; Query Match
Best Local Similarity 28.0%; Prod. No. 3e-10;
Matches 45; Conservative 28; Mismatches 72; Indels 16; Gaps ò g ò g

δγ

Search completed: August 27, 2002, 11:02:53 Job time: 37 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

August 27, 2002, 11:02:21; Search time 11.95 Seconds (without alignments) 648.026 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-821-821-2 1027 1 MDSSTAHSPVFLVFPPEITA.....SLPFSILGCHSEDCDCEQCC 200

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 105224 seqs, 38719550 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Ţ	USE PISCULAR MASCALA	P11836	P13386	SE	z	P13924	E 067062	P07561	P11063	P18931		008746		P48920	P42394	P37784 shigella		P20679	P30628		P18015 clostridiu	ы	996600	NHY P36890 staphylococ	P48762	FU 028851	025578	P24880				EMENT D11628 emericella
SUMM	ID	CD20 MOUSE	CD20_HUMAN	FCEB RAT	FCEB_MOUSE	FCEB_HUMAN	TCR_STRAG	Y917_AQ	TCR_BACST	TCR_STRPN	NU4M_DROME	YAN9_SCHPO	MIN2_MOUSE	NU2M_APILI	NU5M_CHOCR	Y281_BUCAP	RFC_SHIFL	DSBD_PASMU	NU5M_PODAN	VPP1_CAEEL	NU4M_AN	COP_CLOPE	SSPN_MOUSE	YS97_CAEEL	TCR_STAHY	NAH1_PIG	YE21_ARCFU	Y920 HELPY	NU4M_AS	COX1_CAEEL	CAN1_YE	NAH1_BC	NITSMEN
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	Score		169	158	157.5	123.5	98.5	94	91.5	91.5	06	87.5	87.5	86.5	86.5	86	82	82	82	82	84.5	84	84	84	83.5	83.5	83	82.5	82.5	82.5	82.5	82.5	ç
	Result	-	7	٣	4	2	9	7	8	6	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	33

Q9vmw8 drosophila P24881 ascaris suu		P07710 drosophila P34356 caenorhabdi			P08774 neurospora
MPU1_DROME COX1_ASCSU	NAHL RABIT YC38 PORPU Y680 HAFTN	NUIM_DROYA YLHZ CAEEL	CYB_ASCSU CKR2_RAT	NU4M_ANOQU NAH1_HUMAN	NUIM_NEUCR
н н					Н
252	816 291	324	365	448 815	371
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34 35	37	0 6 4 0 0 0	44	43 44	45

ALIGNMENTS

O1-FEB-1991 (Rel. 17, Created) O1-FEB-1991 (Rel. 17, Last sequence update) O1-FEB-1992 (Rel. 17, Last sequence update) O1-MAR-2002 (Rel. 17, Last sequence update) LY-44) MASA-106 (CD20 OR LY-44 OR MS4A2. MASA-106 (CD20 (MS-12)) MASA-106 (MS-12) MASH-2005 (MS-12) MASH-2005 (MS-12) MASH-2005 (MS-12) MASH-2005 (MS-12) MASH-2006 (MS	CD20_M	CD20_MOUSE ID CD20_MOUSE	STANDARD;	PRT;	291 AA	AA.	
Ol-WAR-2002 (Rel. 41, Last annotation update) D-cell surface protein CD20 homolog (B-cell differentiation antigen NS4A1 OR CD20 OR LY.44 OR MS4A2. Mus musculus (Mouse). Muskarydca, Mcazzoa; Chordata; Craniata; Vertebrata; Euteleostom!; Rustarydca; Mcazzoa; Chordata; Craniata; Vertebrata; Euteleostom!; Rusharydca; Mcazzoa; Chordata; Craniata; Vertebrata; Euteleostom!; NCBL_TaxID-10090; Scounce From N.A. MEDLINE-89067519; PubMed-2461992; Teddar T.F., Klejman G., Disteche C.M., Adler D.A., Schlossman S.F., Salto H.;; Klejman G., Disteche C.M., Adler D.A., Schlossman S.F., Cloning of a complementary DNA encoding a new mouse B lymphocyte and localization antigen, homologous to the human B1 (CD20) antigen, and localization antigen, homologous to the human B1 (CD20) antigen, J. Immunol. 141:4388-4394(1988). Salto H.; Klejman G., DibMed-1121785; Medit E., Salto T., Salto T., Shibata K., Yoshino M., Itch M., Ishii Y., Krawa J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y., Krawa J., Shinagawa A., Shibata M., Radach S., Yamanak I., Atawa K., Wasuda H., Kadot K., Matsuda H., Cawa M., Wallin K., Kiyoswa H., Kadot K., Matsuda H., Ashburner M., Batalov S., Yamanak I., Kraya K., Wasuki R., Matalov S., Wamanak I., Kraya M., Wagner L., Washio T., Sahin L., M., Staubil F., Peruno M., Anon H., Baldarelli R., Barsh G., Bolunga M., Baldarelli R., Barsh G., Bolunga M., Barnak J., Bolunga M., Barnak J., Bolunga M., Barnak J., Bolunga M., Barnak J., Bolunga M., Hung B., Khing B.,	N I I		(Rel. 17, Creat (Rel. 17, Last	ed) sequence	updat	(e)	
MS4A1 OR CD20 OR LY 44 OR MS4A2. MS4A1 OR CD20 OR LY 44 OR MS4A2. MS4A1 OR CD20 OR LY 44 OR MS4A2. MS mscallia (Mouse). Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. MSDUNCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-80067319; Pubmed-2461992; Tedder T.F., Klejman G., Disteche C.M., Adler D.A., Schlossman S.F., Salto H.; "Cloning of a complementary DNA encoding a new mouse B lymphocyte differentiation of the gene to chromosome 19."; "Cloning of a complementary DNA encoding a new mouse B lymphocyte differentiation of the gene to chromosome 19."; "Immunol. 141:4388-4394(1988). J. Immunol. 141:4388-4394(1988). STRAIN-C57BL/65; TSUE-Thymus; MSTRAIN-C57BL/66; Pubmed-1121788). STRAIN-C57BL/66; Pubmed-1121788. MASTAIN-C57BL/67; Taxaw A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara M., Shibata K., Yoshino M., Adachi J., Frkuda S., Arakawa T., Hara M., Shibata K., Yoshino M., Adachi J., Frkuda S., Arakawa T., Hara M., Ashburner M., Barlalov S., Casavant T., Salto T., Okazati Y., Golobori T., Bono H., Rasukwa T., Salto R., Arakawa T., Hara M., Ashburner M., Barlalov S., Casavant T., Kabhi P., Lewis S., Matsuo Y., Nikado I., Rasukwa T., dessing M., Schrim L.M., Stabuli F., Suzuki R., Tomita M., Wagner L., Wassho T., Sakai K., Okido T., Putuno M., Aono H., Baldarelli R., Barsh G., Berwisten M.J., Boljunga N., Carninci P., Ge Bonaldo M., Gusnincicola J., Shinashum J., Manbarts P., Kardino P., Lewis S., Malli D., Hofmann M., Hume D.A., Kamilya M., Casnorto P., Rasconto P., Lewis S., Walshum J., Mondone P., Kaning M., Hono B., Sandro N., Gusnint H., Toyo-oka K., Wang K.H., Weiz C., Whittaker M., Shord H., Rabellows D., Schoth M., Schoth M., Waszarelli M., Sato K., Wang K. Mang K.H., Weiz J. Mender A., Wang C., Whittaker M., Schoth M., Shunkahawan J., Shord M., Waszarelli M., Wang C., Whittake	ם	01-MAR-2002 B-cell surfa	(Rel. 41, Last ce protein CD20	annotatio homolog	n upd (B-ce	ate) 11 differentiation a	ntigen
Wis musculus (Wouse) Bukaryota, McLazaoa Chordata; Craniata; Vertebrata; Buteleostomi; MAMMMalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NOBI_TaxID=10090; [1] SEQUENCE FROM N. A. MEDLINE-89067519; PubMed=2461992; Tedder T.F., Klejman G., Disteche C.M., Adler D.A., Schlossman S.F., Salton H.; "Cloning of a complementary DNA encoding a new mouse B lymphocyte differentiation antigen, homologous to the human B1 (CD20) antigen, and localization of the gene to chromosome 19."; I mmunol. 141:4388-4394(1988). STRANHE-STBLE/GSTBL	OE ON	LY-44). MS4A1 OR CD2	0 OR LY-44 OR M	IS4A2.			
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PIR;
PIR;
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REPARAMENTAL STATES OF STATES 
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
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MEDLINE-88124792; PubMed-2448768;
Tedder T.F., Streull M., Schlossman S.F., Saito H.;
"Isolation and structure of a cDNA encoding the B1 (CD20) cell-surface antigen of human B lymphocytes.";
Proc. Natl. Acad. Sci. U.S.A. 85:208-212(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 GSVLFINSGAFLIAVKRKTTETLIILSR-IMNFLSALGAIAGIIL-----LTFGFILD 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 QN------YIC---GYSHQNS----QCKAVTVLFLGILITLMTFSIIELFIS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 MRRLELIQTSKPYVDIYDCEPSNSSEKNSPSTQYCNSIQSVFLGILSAMIJSAFFQKLVT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 TFSTQSPLQKLFARKMKILGTIQILFGIMTFSFGVIFLFTLLKPYPRFPFIFLS-GYPFW 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD20_HUMAN STANDARD, PRT, 297 AA.
P1836; P08984; Q13963;
01-NOV-1988 (Rel. 09, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-OCT-1989 (Rel. 41, Last annotation update)
B-lymphocyte antigen CD20 (B-lymphocyte surface antigen B1) (Leu-16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stamenkovic I., Seed B.; "Analysis of two cDNA clones encoding the B lymphocyte antigen CD20 (Bl, Bp35), a type III integral membrane protein."; J. Exp. Med. 167:1975-1980(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.8%; Score 173; DB 1; Length 291; 29.4%; Pred. No. 2.7e-07; Live 29; Mismatches 64; Indels
                                                                                                 CE BELL; M62541; AAA37394.1; -. REMBL; M62541; AAA37394.1; -. REMBL; AR017903; BAB30996.1; -. REMBL; AR018903; A30558.

RR PIR; A30558; A30558.

RR MGD; MGT:88921; M44a2.

CYTOPLASMIC | 44 CYTOPLASMIC (POTENTIAL).

FT DOMAIN | 1 44 CYTOPLASMIC (POTENTIAL).

RR MGD; MGT:88321; MG4a2.

FT DOMAIN | 1 44 CYTOPLASMIC (POTENTIAL).

RR MGD; MGT:883214.1.

RR MGT:88321; MG4a2.

CYTOPLASMIC (POTENTIAL).

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DF478ECD2C5C16FC CRC64;
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MEDLINE-99176281; PubMed-2466899;
Tedder T.F., Klejman G., Schlossman S.F., Saito H.;
Tedder T.F., Klejman G., Schlossman S.F., Saito H.;
Structure of the gene encoding the human B lymphocyte
differentiation antigen CD20 (B1):",
J. Immunol. 142:2560-2568(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
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MEDLINE-88258386; PubMed-3260267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31958 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53; Conservative
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112
183
204
291 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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Matches
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                             J.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :::| ||: | | :: : : |: || || || || ||:|:||
92 IMYIISGSLLAATEKNSRKCLVKGKMIMNSLSLFAAISGMILSIMDILNIKISHFLKMES 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 STQSPLQKLFARKMKILGTIQILFGIMTFSFGVIFLFTLLKPYPRF-PFIFLSGYPFWGS 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: THIS PROFEIN MAY BE INVOLVED IN THE REGULATION OF B-CELL ACTIVATION AND PROLIFERATION.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- PHM: PHOSPHORYLATED. MIGHT BE FUNCTIONALLY REGULATED BY PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 FGFILDQN-YICGY-----SHQNS----QCKAVTVLFLGILITLMTFSII-ELFIS 181
                             Ledbetter
MEDLINE-88283639; PubMed-2456210;
Einfeld D.A., Brown J.P., Valentine M.A., Clark E.A., Ledbetter
"Molecular cloning of the human B cell CD20 receptor predicts a
hydrophobic protein with multiple transmembrane domains.";
EMBO J. 7:711-717(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63; Indels
                                                                                                                                                                                              KINASE(S).

KINASE(S).

SIMILARITY.

DATABASE: NAME-PROW; NOTE-CD guide CD20 entry;

WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd20.htm".
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> L (IN REF. 4)
-> I (IN REF. 3)
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Pred. No. 5.9e-07;
7; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 AA
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CYTOPLASMIC
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CYTOPLASMIC
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EMBL; M27395; -; NOT_ANNOTATED_CDS.
EMBL; L23415; AAA88911.1; JOINED.
EMBL; L23416; AAA88911.1; JOINED.
EMBL; L23416; AAA88911.1; JOINED.
EMBL; X07203; CAA30180.1; -.
EMBL; X07204; CAA30180.1; -.
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30.3%; Pre-
vative 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X12530; CAA31046.1; -.
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33077
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84
105
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297
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183
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S00387; S00387
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Best Local Similarity
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us-09-821-821-2.rsp

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MEDIINE-89359361; PubMed-2527850; Ra C., Jouvin M.H.E., Kinet J.-P.; "Complete structure of the mouse mast cell receptor for IgE (Fc epsilon RI) and surface expression of chimeric receptors (rat-mouse-
  01-MAR-2002 (Rel. 41, Last annotation update)
High affihity immunoglobulin epsilon receptor beta-subunit (FCERI)
(IGE FC receptor, beta-subunit) (FC epsilon receptor I beta-chain).
MS4A2 OR FCERIB OR FCEIB OR MS4A1.
                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                     human) on transfected cells.";
J. Biol. Chem. 264:15323-15327(1989).
                                                           Mus musculus (Mouse).
                                                                                                     NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                      MEDLINE-88320465; PubMed-2970642;
Kinet J.-P., Blank U., Ra C., White K., Metzger H., Kochan J.;
"Isolation and characterization of Cobns coding for the beta subunit of the high-affinity receptor for immunoglobulin E.";
Proc. Natl. Acad. Sci. U.S.A. 85:6483-6487(1988).
-!- PUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS EPSILON. HIGH AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR BOUND IGE LEADS TO CELL ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQTWQSFLKKELEFLGVTQVLVGLICLCFGTVVCSTLQTSDFDDEVLLLYRAGYPFWGAV 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostoml;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 LFINSGAFLIAVKRKTTETLIILSRIMNFLSALGAIAGIILLTFGFILDQNYICGYSHQN 153
                                                                                                                                                                                                                                                                                      RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSPLQKLFARKMKILGTIQILFGIMTFSFGVIFLFTLLKP--YPRFPFIFLSGYPFWGSV 93
01-JAN-1990 (Rel. 13, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
High affinity immunoglobulin epsilon receptor beta-subunit (FCERI)
(IGE Fo receptor, beta-subunit) (Fc epsilon receptor I beta-chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                ALSO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES. SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO
                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 11-29; 37-43 AND 217-243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 158; DB 1; Length 24., Pred. No. 3.8e-06; T2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL) POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL)
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471DFA59B6688E5D CRC64;
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                                                                                                                                                                                                                                                                                                                            DISULFIDE LINKED GAMMA CHAINS.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE MS4A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 SQCKAVT-----VLFLGILITLMTFSIIELFISLPFSIL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.4%; Scor.
28.0%; Pred. No. J...
28.0%; Mismatches
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                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M22923; AAA41149.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26730
                                                          MS4A2 OR FCERIB OR FCEIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
79
1117
1130
1150
1199
243
                                                                       Rattus norvegicus (Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gE-binding protein;
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Matches 45; Conserv
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                                                                                                                   NCBI_TaxID=10116;
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                 RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOOWD IGE LEADS TO CELL ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE)
RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR ALSO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES.
-!-SUBINIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO DISULFIDE LINKED GAMPA, CHAINS.
-!-SUBCELLULAR LOCATION: Integral membrane protein.
                                                 Hiraoka S., Watanabe M., Takagaki Y., Fujita-Suzuki K., Shinohara N.,
Okumura K., Ra C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 FGIMTESFGVIFLETLLKPY----PRFPFIFLSGYPFWGSVLFINSGAFLIAVKRKTTE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 VGLICLCFGTIVCSVL---YVSDFDEEVLLLYKLGYPFWGAVLFVLSGFLSIISERKNTL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 TLIILSRIMNFLSALGAIAGIILLFFGFILDQNYICGYSHQNSQCKAVT-----VLFL 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The genomic structure of the allergy associated Fc receptor beta
                                                                                                                           subunit and its high content of SINËs.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS EPSILON.
AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27;
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1C2D6BF195738168 CRC64;
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CYTOPLASMIC (POTENTIAL).
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109
122
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Best Local Similarity
Matches 60; Conserv
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SEQUENCE FROM N.A.
                           STRAIN=129;
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TRANSMEM
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235 AA

PRT;

STANDARD;

FCEB_MOUSE

RESULT

(Rel. 17, Created) (Rel. 17, Last sequence update)

01-FEB-1991 01-FEB-1991 FCEB_MOUSE P20490;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT GLY-237.
MEDLINE-96440420; PubMed-8842731;
Shirakawa T., Mao X.-Q., Sasaki S., Enomoto T., Kawai M., Morimoto K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97123518; PubMed-8968765;
Shirakawa T., Mao X.-Q., Sasaki S., Enomoto T., Kawai M., Morimoto K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hum. Mol. Genet. 5:2068-2068(1996).
-1- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS EBSILON. HIGH
AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC
RESPONSE. BINNING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL
ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and a coding variant of Fc-epsilon-
MEDLINE-92316966; PubMed-1535625; Kuester H., Zhang L., Brinl A.T., Macglashan D.W., Kinet J.-P.; Thest ene and CDNA for the human high affinity immunoglobulin E receptor beta chain and expression of the complete human receptor."; J. Biol. Chem. 267:12782-12787(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDILINE=96414302; PubMed-8817330;
Hill M.R., Cookson W.O.;
"A new variant of the beta subunit of the high-affinity receptor for
immunoglobulin E (Fc epsilon RI-beta E237G): associations with
measures of atopy and bronchial hyper-responsiveness.";
Hum. Mol. Genet. 5:959-962(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR ALSO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES. SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO
                                                                                                                                                                                     01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
High affanity immunoglobulin epsilon receptor beta-subunit (FCERI)
(IGE Fc receptor, beta-subunit) (Fc epsilon receptor I beta-chain).
                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maekawa K., Imagawa N., Tanaka Y., Harada S.;
"Determination of the sequence coding for the beta subunit of the human high-affinity IgE receptor.";
FEBS Lett. 302:161-165(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFIDE LINKED GAMMA CHAINS.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: FOUND ON THE SURFACE OF MAST CELLS AND
                                                                                                                                                         244 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Association between atopic asthma all beta in a Japanese population."; dum. Mol. Genet. 5:1129-1130(1996).
                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92339505; PubMed-1386024;
|: | | : | : | : | 117 YLVRGSLGANIVSSIAAGTGIAMLIL-
                                            165 GILITLMTFSIIELFIS 181
                                                                          170 TELVLMMLFLTILAFCS 186
                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                      MS4A2 OR FCER1B
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Nucleic Acids Res. 17:7283-7294(1989).
-i- FUNCTION: RESISTANCE TO TETRACYCLINE EFFLUX. THIS IS AN BIRRGY-DEPENDENT PROCESS THAT DECREASES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 TVVCSVLDISHIEGDIFSSFKAGYPFWGAIFFSISGMLSIISERRNATYLVRGSLGANTA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 VIFLFTLLKPYPRFPFI--FLSGYPFWGSVLFINSGAFLIAVKRKTTETLIILSRIMNFL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SALGAIAGIILLTFGFILDQNYICGYSHQNS-----QCKAVTVLFLGILITLMTF-SIIE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 PAFEVL--EISPQEVSSGRLLKS--ASSPPLHTWLTVLKKEQEFLGVTQILTAMICLCFG 76
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 244;
                                                                                                                                                                                                                                           Transmembrane; Polymorphism.
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.0%; Score 123.5; DB 1; 25.6%; Pred. No. 0.0023; tive 33; Mismatches 93;
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TCR_STRAG
191324;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
10. 130, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                         FTIG=VAR_003965.
                                                                                                           or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                           Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            26533 MW;
                                                                                                                                           EMBL; D10583; BAA01440.1; -. EMBL; M89796; AAA60269.1; -. PIR; S21154; S21154. PIR; A42806.
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79
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244
237
                                                                                                                                                                                                                                       IgE-binding protein;
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DOMAIN
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TCR_STRAG
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                                                                                                                                                                                                                      MIM;
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Best Local Similarity
Matches 52; Conserv
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                                                                                                                                                                                                                                                                                                                                                            145
180
236
270
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                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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ACCUMULATION OF THE ANTIBIOTIC IN WHOLE CELLS. THIS PROTEIN FUNCTIONS AS A METAL-TETRACYCLINE/H+ ANTIPORTER.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN AS THE DRUG RESISTANCE TRANSLOCASE FAMILY).
                                                                                                                                                                                                                                                                                                                                                                                                      ic resistance; Transmembrane; Transport; Symport; Plasmid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68; Indels
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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NCBI_TaxID=63363;
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                                                                                                                                                                                                                                                                                       Mabi, Allows, PTSOG, 1R, C2569); YTSOG, InterPro; IPR001411; TCR_TetB. InterPro; IPR003662; sub_trans
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Pfam; PF00083; sugar_tr; 1.
PRINTS; PR01036; TCRTETB.
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Best Local Similarity 25,99
Matches 45; Conservative
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458 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 -SLLYISS---IMLYK-----LLRIKNLRDAPRGFRFALGSFTAGIILATFLVLNL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FGFI-LDQNY-----NSQCKAVTVLF 163
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-!- FUNCTION: RESISTANCE TO TETRACYCLINE BY AN ACTIVE TETRACYCLINE
EFFLUX. THIS IS AN ENERGY-DEPENDENT PROCESS THAT DECREASES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-86031344; PubMed-2996983;
Puboshino T., Ikeda T., Tomizuka N., Furukawa K.;
"Nucleotide sequence of the tetracycline resistance gene of pTHTLE
thermophilic Bacillus plasmid: comparison with staphylococcal TCR
Nature 392:353-358(1998).
-I- SUBCELLUTAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : ||:| | | || || 79 EDPLKKATFVHIGLTLGTLELVYGLYSFNKVALLGLFFLLI----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.2%; Score 94; DB 1; Length 408; 25.6%; Pred. No. 0.88; Live 24; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                              EMBL; AE000713; AAC07022.1; -.
Hypothetical protein; Transmembrane; Complete proteome
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01-APR-1988 (Rel. 07, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
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MEDLINE=87226167; PubMed=2438417;
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                                                                                                                                                                                                                                                                                                                                                                                                          TFSTQSPLQKLFARKMKILGTIQILFGIMTFSFGVIFLFTLLKPYPRFPFIFLSGYPFWG 91
ACCUMULATION OF THE ANTIBIOTIC IN WHOLE CELLS. THIS PROTEIN FUNCTIONS AS A WETAL-TETRACYCLINE/H+ ANTIPORTER. SUBCELLULAR LOCATION: Integral membrance protein. SIMILARITY: BELONGS TO THE MAJOR FACTLITATOR FAMILY (ALSO KNOWN AS THE DRUG RESISTANCE TRANSLOCASE FAMILY).
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                                                                                                                                                                       InterPro; IPR003662; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
PRINTS; PR01036; TCRTETB.
Antibiotic resistance; Transmembrane; Transport; Symport; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                       224 SFLIVSVLSFLIFVKHIRKVTDPFVDPGLGKNIPFMIGVLCGGIIFGTVAGFVSMVPYMM
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                                                                                                                                                                                                                                                                                                                                                                     Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 KDVHQLSTAEIGSVIIFPGTMSVIIFGYIGGILVDRRGPLYVLNIGVTFLSVSF
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25.3%; Pred. No. 1.6;
Live 26; Mismatches
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SEQUENCE FROM N.A.
SPECIES-S.pneumoniae; PLASMID-PLS].
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162
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458 AA;
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MEDLINE-86287699; PubMed-3090576;

MEDLINE-86287699; PubMed-8628769;

MEDLINE-86287699; PubMed-8628769;

MEDLINE-8628769; PubMed-8628769;

MEDLINE-8628769; PubMed-8628769;

MEDLINE-8628769; PubMed-8628769;

MEDLINE-8628769; PubMed-8628769;

MEDLINE-8628769; PubMed-8628769;

MEDLINE-8628769; PubMed-3090576;

MEDLINE-86
Lacks S.A., Lopez P., Greenberg B., Espinosa M.; "Identification and analysis of genes for tetracycline resistance and replication functions in the broad-host-range plasmid pLSI."; J. Mol. Biol. 192:753-765(1986).
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"The origin of replication of plasmid P15A and comparative studies on
the nucleotide sequences around the origin of related plasmids.";
Cell 32:119-129(1983).
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"New Shuttle vectors for Escherichia coll and Bacillus subtilis. III.
Noclectide sequence analysis of tetracycline resistance gene of
pAMalphal and ori-177."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Palva A., Vidgren G., Simonen M., Rintala H., Laamanen P.;
"Nucleotide sequence of the tetracycline resistance gene of pBC16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES-B.subtilis; PLASMID-PTB19; MEDLINE-92052681; PubMed=1946749; Oskam L., Hillenga D.J., Venema G., Bron S.; The large Bacillus plasmid pTB19 contains two integrated rolling-circle plasmids carrying mobilization functions."; Plasmid 26:30-39(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from Bacillus cereus.";
Nucleic Acids Res. 18:1635-1635(1990).
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InterPro; IPR003662; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
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EMBL; M29725; AAA98167.1; -.
EMBL; D13792; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                              SPECIES-B.cereus; PLASMID=PBC16;
MEDLINE-90221899; PubMed-2109312;
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MEDLINE=83129391; PubMed=6186390;
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EMBL; D00006; BAA00005.1; -.
PIR; S09214; YTBSU6.
PIR; C25599; YTSOG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                        92 SVLFINSGAFLIAVK - - RKTTETLIILSRIMNFLSALGAIAGIILL - - TFGFILDQNYIC 147
                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Drosophila melanogaster mitochondrial DNA: gene organization and evolutionary considerations.";
Genetics 118:649-663(1988).
                                                                                                                                                                                                                                                              Transmembrane; Transport; Symport; Plasmid
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                                                                                                                                                                                                                                                                                                      284 KDVHQLSTABIGSVIIFPGTMSVIIFGYIGGILVDRRGPLYVLNIGVIFLSVSF 337
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                                                                                                                                       6A708777D44C2074 CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3).
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25.3%; Pred. No. 1.6;
tive 26; Mismatches
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FlyBase, FBGN0013682; mt:ND4.
InterPro; IPR003918; NADHUb.oxdrdctse4.
InterPro; IPR001750; Oxidored_q1.
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EMBL; U37541; AAC47819.1; -.
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MEDLINE-88212147; PubMed=3130291;
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  PR01036; TCRTETB.
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458 AA;
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Gentles S., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
-I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-I- SIMILARITY: TO YEAST YKL146W AND YNL101W.
                                                                                                                                                                                                                                                                                                                                                                                                                                46 SEISYFIGCDMISYGLILLSLWICKLMALASEMINKHNNYKNLFLLNIILLLLLLILTFF 105
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                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                   40;
Pfam; PF00361; oxidored_q1; 1.
Pfam; PF01059; oxidored_q5 N; 1.
PRINTS; PR01437; NUOXDRDTASE4.
Oxidoreductase; NB; Ubiquinone; Mitochondrion.
CONFLICT 161 161 S -> V (IN REF. 1; AAC47819).
SEQUENCE 446 AA; 51371 MW; BAB4A98563238BB2 CRC64;
                                                                                                                                                                                               Length 446;
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7FD1E8F649ED83D2 CRC64;
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30-MAY-2000 (Rel. 39, Last annotation update)
Hypothetical 73.1 kDa protein C3H1.09C in chromosome SPAC3H1.09C.
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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8.8%; Score 90; D

Best Local Similarity 23.6%; Pred. No. 2;

Matches 34; Conservative 25; Mismatche
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PF01490; Aa_trans; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Perimary structure and expression of matrilin-2, the closest relative of cartilage matrix protein within the von Willebrand factor type A-like module superfamily.

J. Biol. Chem. 272:9268-9274(1997).

I. Sid. Chem. 272:9268-9274(1997).

Subcritor: INVOLVED IN MARIEX ASSEMBLY (BY SIMILARITY).

Subccellular LOCATION: Secreted.

I. TISSUE SPECIFICITY: DETECTED IN A VARIETY OF ORGANS, INCLUDING CALVARIA, UTERGY, HEART, AND BRAIN, AS WELL AS FIBROBLAST AND GSTEOBLAST CELL LIRES.

SIMILARITY: CONTAINS 10 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 2 VWFA DOMAINS.
                                                                  | | : : | : --LIADVFILLGILXLYFWDVITLATKGIAD 448
                                                                                                                                        SGAFLIAVKRKTTETLIILSR------IMNFLSALGAIAGIILLTFG--FILDQNYICG 148
                              Gaps
                                                                                                          449 VAMFNKTDFSLFIGVAIFTYEGICLILPIQEQMAKPKNLPK----LLTGVMAAISLLFIS 504
                                                                                                                                                      ---TLLKP--YPRFPFIFLSGYPFWGSVLFIN 97
                                                                                                                                                                                    149 YSHQNSQCK-----AVTVLFLGILITIMIFSIIELFISLFFSILGCHSEDCDCEQCC 200 :| : | | | : | | : | | | : | |
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                 565 SGKRNRKIKWRKNYLRVLIVILAILISWAGSSRLDLFVSMVGSV------CC
                              75;
       Length 656;
                                               11 FLVFPPEITASEYESTELSATTFSTQSPLQKLFARKMKILGTIQILF----
                            75; Indels
        DB 1;
                                                                                                                                                                                                                                                                                       (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 39, Last annotation update)
                           34; Mismatches
       Score 87.5;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:109613; Matn2.
InterPro; IPR000152; Asx.lhydroxyl.
InterPro; IPR00152; BGF-like.
InterPro; IPR001881; BGF_Ca.
InterPro; IPR002035; vWFA.
Ffan; PF00008; BGF; 10.
Pfan; PF000092; vwa; 2.
                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BALB/C; TISSUE-Limb;
MEDLINE-97238863; PubMed-9083061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ļ.
                                                                      400 FLVFVP--LSLVRKISKLSATA----
                                                                                            58 -----GIMTFSFGVIFLF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0453; VARFADOMAIN.
SMART; SMO0181; EGF; 10.
SMART; SMO0327; VWA; 2.
PROSITE; PS00010; ASX_HYDROXYL;
     8.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U69262; AAC53163.1; -. HSSP; P35555; 1EMN.
                Best Local Similarity 22.7 Matches 54; Conservative
                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                          Matrilin-2 precursor.
                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 30-MAY-2000
                                                                                                                                                                                                                                                                                        30-MAY-2000
                                                                                                                                                                                                                                           RESULT 12
MTN2_MOUSE
ID MTN2_MOUSE
     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 ILSRI----MNFLSALGA--IAGIILLTFGFILDQNYICGYSHQNSQCKAVTVLFLGILI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 --FSFGVIF----LFTLLKPYPRFPFIFLSGYPFWGSVLFINSGAFLIAVKRKTTETLI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 FLVFPPEIT---ASEYEST---ELSATTFSTQSPLQKLFARKMKILGTIQILFGIMT--- 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 TLMTFSIIE-----LFISLPFS-----ILG-------CHSEDCDCEQCC 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL);
384C22770B6E6EEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.5%; Score 87.5; DB 1; Length 956; 23.2%; Pred. No. 6.4; Live 31; Mismatches 76; Indels 7?
; EGF_2; 9.
; VWFA; 2.
Signal; Glycoprotein; Repeat; Coiled coil.
                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                              COLLED COLL (POTENT
BY SIMILARITY.
                                                                                                            EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 6.
EGF-LIKE 6.
EGF-LIKE 7.
EGF-LIKE 7.
EGF-LIKE 9.
EGF-LIKE 9.
EGF-LIKE 9.
                                                                           MATRILIN-2.
                                                            POTENTIAL.
                                                                                              VWFA
                                                                                                                                                                                                                                                                                                    VWFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106779 MW;
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                                                                                                                                                                                                                                                                                                                                                                                       294
303
318
335
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33.54
33.54
33.54
33.54
44.10
55.08
55.08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 55; Conserv
                                      EGF-like domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arias M.C., Sheppard W.S.;
Molecular phylogenetics of honey bee subspecies (Apis mellifera L.)
inferted from mitochondrial DNA sequence.";
Mol. Phylogenet. Evol. 5:557-566(1996).
                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
Apoidea; Apidae; Apis.
NCBI_TaxID=7469;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Crozier R.H., Crozier Y.C.; The mitochondrial genome of the honeybee Apis mellifera: complete sequence and genome organization."; Genetics 133:97-117(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-HAPLOTYPES 1 TO 11;
Koulianos S., Crozler R.H.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
-! - CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-! - SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
        RESULT 13
NUZM_APILI STANDARD; PRT; 333 AA.

LO NUZM_APILI STANDARD; P92502; P92886; P92907; Q33786; Q33786; Q33787; Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
                                                                                                                                                                                                                       Apis mellifera ligustica (Common honeybee) Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93114603; PubMed=8417993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=VARIOUS STRAINS;
MEDLINE=96364025; Pubmed=8744768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, 106178; AAB96798.1; EMBL, 035743; AAB38223.1; EMBL, 035746; AAB38223.1; EMBL, 035746; AAB38225.1; EMBL, 035746; AAB38225.1; EMBL, 035748; AAD12744.1; EMBL, 035749; AAB38228.1; EMBL, 035750; AAB38228.1; EMBL, 035752; AAB38228.1; EMBL, 035752; AAB38223.1; EMBL, 035752; AAB38230.1; EMBL, 035753; AAB38230.1; EMBL, 035753; AAB38230.1; EMBL, 035753; AAB38230.1; EMBL, 035753; AAB38230.1; EMBL, 035754; AAB38230.1; EMBL, 035754; AAB38230.1; EMBL, 035754; AAB38230.1; EMBL, 035754; AAB38232.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 60-307 FROM N.A.
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AAB38235.1;
AAB38236.1;
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AAB38242.1;
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EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----IFLF-TLLKPYPRFPFIFLSGYPFWGSVLFINSGAFL--IAVKRKTTETLIILSRI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 MN----FLSALGA---IAGIILLTFGFILDQNYICGYSHQNSQCKAVTVLFLGILITLM 171
                                                                                                                                                                                                                                                                                                                                                                                                                                               SPVFLVFPPEITASEYESTELSATTFSTQSPLQKLFARKMKILGTIQILFGIMTFSFGV- 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Rhodophyta; Florideophyceae; Gigartinales; Gigartinaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Apices;
MEDLINE-95341681; PubMed-7616569;
Leblanc C., Boyen C., Richard O., Bonnard G., Grienenberger J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             666 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chondrus crispus (Carragheen).
          AAB41177.1;
AAB41177.1;
AAB41178.1;
AAB41179.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 -TFSIIELFIS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :|: :|:|
FNYSMYPIFLS 248
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                     U72279;
U72280;
U72281;
U35764;
U35765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitochondrion
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P48920;
                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
NU5M_CHOCR
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153 ILALLLALLSHAVIYVECQKKSCNVSVITFNALPSLISGIFLSIISWFIESP 204
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Job time: 183 sec
                                                                                                                                                                                                                                                           EMBL; Z19055; CAA79502.1; -
Interpro; IPR000620; DUF6.
Pfam; PF00892; DUF6; 2.
Hypothetical protein; Transpo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
           S. TYPHIMURIUM PAGO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
TRANSMEM
TRANSMEM
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TRANSMEM
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           8
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                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 453 NLAKSSINLVHESSLIMIFPLIILSIGSTFAGYLIRDLFVGSGSDFWGAAIFILPKHSTF 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394 PFLTGFYSKDFILELTQISSYSNLQMSYISFACWLGTMSVFF-TSFYSFRLIYLTFLNNT 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---CGYSHQNS------QCKAVTVLFLG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            573 LYNRLIVLPILNEGYSISFKILDRGFIELSGPYGFTKFVSFWSQILIKLQTGQITHYLFF 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 PEITASEYESTELSATTFSTQSPLOKLFARKMKILGTIQILFGIMTFSFGVIFLFTLLKP 75
                                                                                                      J. Mol. Biol. 250:484-495(1995).
-I- CATALYTIC ACTIVITY: NADH + ACCEPTOR = NAD(+) + REDUCED ACCEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
MEDIJOR-94012512; PubMed-8407819;
Munson M.A., Baumann P.;
"Molecular cloning and nucleotide sequence of a putative trpDC(F)BA operon in Buchnera aphidicola (endosymbiont of the aphid Schizaphis

    -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
    -1- SIMILARITY: BELONGS TO THE EAMA TRANSPORTER FAMILY. STRONG, TO

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----SGXPFWGSVLFINS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -------GAFLIAVKRTTETLIILSRIMNFLS-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93;
Kloareg B.; "Complete sequence of the mitochondrial DNA of the rhodophyte Chondrus crispus (Gigartinales). Gene content and genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 666 AA; 75628 MW; 37EB6F2C24B9D360 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-NOV-1995 (Rel. 32, Last sequence
10-NOV-101 (Rel. 40, Last annotation update)
Hypothetical protein BU281 homolog
Buchhera aphidicola (subsp. Schizaphis graminum).
Bacteria: Protecbacteria; gamma subdivision; Buchnera.
NCBI_TaxiD=98794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.4%; Score 86.5; D
20.8%; Pred. No. 5.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003916; NADBub oxdrdctse5.
InterPro; IPR001750; Oxidored_q1.
InterPro; IPR001516; Oxidored_q1.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Bacteriol. 175:6426-6432(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 ALGAIAGIILLTFGF----ILDONYI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00361; oxidored_q1; 1.
Pfam; PF00662; oxidored_q1_N; 1.
PRINTS; PR01434; NADHDHGNASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 ILITLMTFSIIEL -- FISLPFSIL 187
                                                                                                                                                                                                                                                                                                                                                                                       EMBL; 247547; CAA87625.1; -.
Mendel; 7732; CHOcr;nad5;1.
                                                                                                                                                                                                                                                                                                                                                                                                                CHOcr; nad5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 20.8%
Matches 55; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 SGAFLIAVKRKTTETLII----LSRIMNFLSALGAIAGIILLTFGFILDQNYICGY---- 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 FATGIRFLAASPLLIILSYLTKKPLLFPYGQRRFQIFISIFYFSIPFTLMLYGGS--YVN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 FSFGVIFLFT-----WGSVLFIN 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 -----SH-----QNSQCKAVTVLF--LGILITLMTFSIIELFISLP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.4%; Score 86; DB 1; Length 300; 25.6%; Pred. No. 2.9; tive 17; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL. F614A9F4D2FA63F6 CRC64;
                                                                                                                                                                                                                                                               Transport; Transmembrane.
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

August 27, 2002, 11:02:16; Search time 19.84 Seconds (Without alignments) 968.642 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-821-821-2 1027 1 MDSSTAHSPVFLVFPPEITA.....SLPFSILGCHSEDCDCEQCC 200

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283138 Total number of hits satisfying chosen parameters: 283138 seqs, 96089334 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	t peasonana aitset	IdE receptor heta	B-cell surface ant	B-cell surface ant	44		IgE Fc receptor be	hypothetical prote			probable transmemb	probable inorganic	hypothetical prote	conserved hypothet	hypothetical prote					tetracycline resis	tetracycline resis			hypothetical prote	_		Þ	probable protein e	
SUMMARIES	O.	JC7585	2	A30558	A30586	A31231	B34342	A42806	C86844	T16070	JH0751	E81306	T07892	F69208	B71315	C70379	E95155	H98021	T01124	T07894	YTBSRT	YTBSU6	YTSOG	JQ1211	A05235	T22748	T37205	S01187	A71514	н70193
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	Query Match Length	200	214	291	297	243	235	244	307	455	152	387	537	165	991	408	439	439	542	533	458	458	458	458	288	1431	457	446	0	244
dР	Query Match	100.0	17.7	16.8	16.5	15.4	15.3	12.0	10.3	10.0	9.7	9.3	9.3	9.3	9.5	9.5	9.5	9.5	9.1	٠	•	٠	6.0	•	•		•	8.8	8.7	8.7
	Score	1027	181.5	173	169	158	157.5	123.5	106	103	100	96	95.5	95	94.5	94	94	94	93.5	92.5	91.5	91.5	91.5	91.5	91	91	90.5	90	89.5	68
	Result No.	н	7	Э	4	ιΩ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

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hypothetical prote sugar permease (im probable inorganic probable inorganic probable inorganic phosphate transpor hypothetical prote L-asparagine perme L-asparagine perme hypothetical prote probable cation ef major facilitator hypothetical prote secDF protein hypothetical prote shopothetical prote hypothetical prote hypothetical prote shopothetical prote hypothetical prote	ALIGNMENTS	1 Homo sapiens (man) 10-2001 disequence_revision 30-Jun-2001 ftext_change 30-Jun-2001 10-10-2001 disequence_revision 30-Jun-2001 ftext_change 30-Jun-2001 10-10-10-2001 disequence_revision 30-Jun-2001 ftext_change 30-Jun-2001 10-20-20-20-20-20-20-20-20-20-20-20-20-20
142971 H96981 T05714 T07164 T07164 T07604 E69143 E98261 H69160 H69160 H69160 H69160 H69160 H69160 H69160 H69160 H89831	ALIGN	transmembrane-4 protein, TETM4 - apiens (man) 01 #sequence_revision 30-Jun-200 85 89 agler, E.; Hornby, J.R.; Hogarth Res. Commun. 280, 374-379, 2001 n, tissue distribution, and chron r: JC7585; MUID:21092614; PMID:10 mRNA GHUL. s: GB:AF321127 rotein, a four-transmembrane pro- rotein, a four-transmembrane fistatus predicted // ransmembrane #status predicted
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8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		ESULT 1 C7585 estis expressed transmembrane- iSpecies: Homo Sapiens (man) iAccession: JC7585 iHulett, M.D.; Pagler, E.; Hor icohem. Blophys. Res. Commun. iTitle: Isolation, tissue dist. Reference number: JC7585; MuI Accession: JC700 (HUL) Comment: This protein, a four iGenetics: Genetics: Genetic
01000000000000000000000000000000000000		RESULT 1 JG7585 testis expressed transmembrane- C; Species; Hono Sapiens (man) C; Date: 30-Jun-2001 #sequence_C; C; Accession: JG7585 R; Holett, M.D.; Pagler, E.; Hor B; Holett, M.D.; Pagler, E.; Hor A; Residues: J-200 <hul> A; Residues: 1-200 <hul> A; Residues: 1-200 <hul> A; Genetics: GB:AF321127 C; Comment: This protein, a four C; Genetics: A; Genetics: C; Genetics: Signal transduction F; J4 Poromain: Ortoplasmic #star F; J4 Poromain: cytoplasmic #star F; Holonain: transmembrane F; Hol-118/Domain: transmembrane F; Hol-118/Domain: transmembrane F; Hol-118/Domain: cytoplasmic #star F; Hol-118/Domain: cytoplasmic #star F; Hol-182/Domain: Hansmembrane F; Hol-182/Domain: cytoplasmic #star F; Hol-182/Fillillillillillillillillillillillillill</hul></hul></hul>

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A.Cross-references: GB:M27394; GB:J03574; NID:g179307; PIDN:AAA35581.1; PID:g179308
B.E. Enfeld, D.A.; Brown, J.P.; Valentine, M.A.; Clark, E.A.; Ledbetter, J.A.
EMBO J. 7, 711-717, 1988
A.Title: Molecular cloning of the human B cell CD20 receptor predicts a hydrophobic p
A;Reference number: S00387; MUID:88283639
A;Accession: S00387
A;Molecule type: mRNA
A;References: EMBL:A07203; NID:g29775; PIDN:CAA30179.1; PID:g29776
A;Experimental source: Daudi cells
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A; Residues: 1-297 <STA>
A; Coss-references: GB:X12530; NID:929773; PIDN:CAA31046.1; PID:929774
A; Cross-references: GB:X12530; NID:929773; PIDN:CAA31046.1; PID:929774
B; Tedder, T.F.; Streuli, M.; Schlossman, S.F.; Saito, H.
Proc. Natl. Acad. Sci. US.A. 85, 208-212, 1988
A; Title: Isolation and structure of a cDNA encoding the B1 (CD20) cell-surface antige A; Recession: A27400
A; Accession: A27400
A; Molecule type: mRNA
A; Residues: 1-297 <TE2>
                                                                                                                                                                                                                                                                                                                   B-cell surface antigen CD20 - human
N;Alternate names: B-lymphocyte antigen CD20; B1
C;Species: Homo saplans (man)
C;Date: OB-Jun-1989 #sequence_revision 02-aug-1996 #text_change 22-Jun-1999
C;Accession: A30586; JL0042; A27400; S00387
R;Tedder, T.F.; Klejman, G.; Schlossman, S.F.; Saito, H.
J:Immunol. 142, 2560-2568, 1989
A;Tille: Structure of the gene encoding the human B lymphocyte differentiation antige A;Reference number: A30586; MUID:89176281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Comment: This protein appears not to be glycosylated. Isoforms of varying molecular C;Comment: This protein plays an important role in B cell activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-297 <TED>
A; Note: the authors translated the codon ATG for residue 148 as His, TCA for residue
b, and GAC for residue 294 as Ser
R; Stamenkovic, I.; Seed, B.
J. Exp. Med. 167, 1975-1980, 1988
A; Title: Analysis of two cDNA clones encoding the B lymphocyte antigen CD20 (B1, Bp35)
A; Réference number: JL0042; MUID: 88258386
A; Reference number: JL0042
---YIC---GYSHQNS----QCKAVTVLFLGILITLMTFSIIELFIS 181
                                                                                                                                        143 MRRLELIQTSKPYVDIYDCEPSNSSEKNSPSTQYCNSIQSVFLGILSAMLISAFFQKLVT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 STQSPLOKLFARKMKILGTIQILFGIMTFSFGVIFLFTLLKPYPRF-PFIFLSGYPFWGS 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 297;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.5%; Score 169; DB 1; 30.3%; Pred. No. 3.4e-08; tive 27; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;186-212/Domain: transmembrane #status predicted F;213-297/Domain: intracellular #status predicted F;167-183/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GDB:119761; OMIM:112210
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C, Superfamily: B-cell surface antigen CD20
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N.Alternate names: B-cell differentiation antigen Ly-44
C; Species: Mus musculus (house mouse)
C; Deccios: Ol-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 07-Feb-1997
C; Accession: A30558
R; Tedder, T.F.; Klejman, G.; Disteche, C.M.; Adler, D.A.; Schlossman, S.F.; Saito, H.
J. Immunol. 141, 4388-4394, 1988
A; Title: Cloning of a complementary DNA encoding a new mouse B lymphocyte differentiatic
A; Reference number: A30558; MUID:8906/519
                                                                                                                                                      R;Adra, C.N.; Lelias, J.M.; Kobayashi, H.; Kaghad, M.; Morrison, P.; Rowley, J.D.; Lim, Proc. Natl. Acad. Sci. U.S.A. 91, 10178-10182, 1994
A;Title: Cloning of the CDNA for a hematopoletic cell-specific protein related to CD20
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                                                                    C.Species: Homo sapiens (man)
C.bate: 31-May-1996 #sequence_revision 31-May-1996 #text_change 05-Nov-1999
C.Accession: I59258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 NSFGMNIASATIALVGTAFLSLNIAVNIQSLRSC---HSSSESPDLCNYMGSISNGMVSL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSVLFINSGAFLIAVKRKTTETLIILSR-IMNFLSALGAIAGIIL-----LTFGFILD 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTFSFGVIFLFTLLKPY --- PRFPFIFLSGYPFWGSVLFINSGAFLIAVKRKTTETLII 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSRIMNFLSALGAIAGIILLTFGFILDQNYI--CGYSHQNSQ----CKAVTVLFLGILIT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----PINGSPDYQK---AKLQVLGAIQILNAA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDSSTAH-SPVFLVFPPEITASEYESTELSATTFSTQSPLQKLFARKMKILGTIQILFGI 59
                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-214 <RES>
A;Cross-references: GB:L35848; NID:9561638; PIDN:AAA62319.1; PID:9561639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25;
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C;Superfamily: B-cell surface antigen CD20
C;Keywords: membrane protein; phosphoprotein; surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                  IgE receptor beta chain / CD20 antigen homolog - human
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16.8%; Score 173; DB 2;
Best Local Similarity 29.4%; Pred. No. 1.4e-08;
Matches 53; Conservative 29; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 17.7%; Score 181.5; DB 2
Best Local Similarity 28.2%; Pred. No. 1.7e-09;
Matches 59; Conservative 38; Mismatches 87
                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Status: not compared with conceptual translation Molecule type: mRNA
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                                                                                                                                                                                                                                                                                       A; Reference number: 159258; MUID:95024008
A; Accession: 159258
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11 LGSASAHGTPGSETGPEELNTSVYH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 11q12-11q13.1
C; Keywords: immunoglobulin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: GDB:CD20L; HTM4
A;Cross-references: GDB:392702
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Residues: 1-291 <TED>
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Inge Fc receptor beta chain - human

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 08-Oct-1999

C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 08-Oct-1999

C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 08-Oct-1999

C;Date: 10-May-1994 #sequence_revision 19-May-1994 #text_change 08-Oct-1999

C;Date: 10-May-1994 #sequence_revision 19-May-1994 #text_change 08-Oct-1999

C;Date: 10-May-1994 #sequence on 19-May-1994 #text_change 08-Oct-1999

A;Faters: The gene and cDNA for the human high affinity immunoglobulin E receptor beta A;Faters: preliminary

A;Molecule type: DNA

A;Faters: preliminary

A;Hoross: references: GB:M89796; NID:9337417; PIDN:AAA60269.1; PID:9337418

R;Maekava, K.; Imagawa, N.; Tanaka, Y.; Harada, S.
FEBS Lett. 302, 161-165, 1992

A;Title: Determination of the sequence coding for the beta subunit of the human high-A;Reference number: S21154; MUID:92339505

A;Actatus: preliminary

A;Actatus: Diffininary

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hypothetical protein ysbC [imported] - Lactococcus lactis subsp. lactis (strain IL140 c); Specials: Lactococcus lactis subsp. lactis
C; Specias: Lactococcus lactis subsp. lactis
C; Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C; Accession: C86844
R; Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Bh Genome Res. 11, 731-753, 2001
A; Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis A; Reference number: A86625; MUID: 21235186; PMID: 11337471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:D10583; NID:g219881; PIDN:BAA01440.1; PID:d1001914; PID:g21988 A;Cross-references: GB:D10583; NID:g21983; 179/3; 212/3 A;Introns: 19/2; 62/3; 107/3; 126/3; 179/3; 212/3 C;Keywords: immunoglobulin receptor; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 PAFEVL--EISPQEVSSGRLLKS--ASSPPLHTWLTVLKKEQEFLGVTQILTAMICLCFG 76
                                                                                          VGLICLCFGTIVCSVL---YVSDFDEEVLLLYKLGYPFWGAVLFVLSGFLSIISERKNTL 116
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                                                           112 TLIILSRIMNFLSALGAIAGIILLTFGFILDQNYICGYSHQNSQCKAVT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 25.6%
Matches 50; Conservative
                                                                                                                                                                                                                        165 GILITLMTFSIIELFIS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 LFISLPFSILGCHSE 192
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LGSAVSLTICGAGEE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-244 <MAE>
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A; Status: preliminary
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C; Species: Mus musculus (house mouse)
C; Species: Mus M. H.E.; Kinet, J. P.
R; Ra, C.; Jouvin, M. H.E.; Kinet, J. P.
J. Biol. Chem. 264, 15323-15327, 1989
J. Biol. Chem. 264, 15323-15327, 1989
J. Rich (complete structure of the mouse mast cell receptor for IgE (Fc-epsilon-RI) & Fitle: Complete structure of the mouse mast cell receptor for IgE (Fc-epsilon-RI) & Fitle: Complete structure of the mouse mast cell receptor for IgE (Fc-epsilon-RI) & Fitle: Complete structure of the mouse mast cell receptor in B4342
A; Reference number: A34342; MuID:89359361
A; Status: Preliminary
A; Molecule type: mRNA
A; Residues: 1-235 cRAC>
A; Cross-references: GB: J05019; NID:q193238; PIDN:AAA37601.1; PID:g309225
C; Keywords: immunoglobulin receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                    Alloading of the perceptor beta chain - rat
C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 05-Nov-1999
C; Accession: A31231
R; Kinet, J. P.; Blank, U.; Ra, C.; White, K.; Metzger, H.; Kochan, J.
Proc. Natl. Acad. Sci. U.S.A. 85, 6883-6887, 1988
A; Title: Isolation and characterization of cDNAs coding for the beta-subunit of the PA; Reference number: A31231
A; Reference number: A31231
A; Reference number: A31231
A; References: A1231
A; Rocession: A31231
A; Rocession: A31231
A; Rocession: A31231
C; Reywords: I-243 KINA
C; Keywords: immunoglobulin receptor; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFINSGAFLIAVKRKTTETLIILSRIMNFLSALGAIAGIILLTFGFILDQNYICGYSHQN 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                           .----T 136
                                                                                                             92 IMYIISGSLLAATEKNSRKCLVKGKMIMNSLSLFAAISGMILSIMDILNIKISHFLKMES 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 QSPLQKLFARKMKILGTIQILFGIMTFSFGVIFLFTLLKP--YPRFPFIFLSGYPFWGSV 93
            36 SLVGPTQSFFMRESKTLGAVQIMNGLFHIALGGL----LMIPAGIYAPICVTVWYPLWGG 91
                                                                                                                                                                                        137 FGFILDQN-YICGY-----SHQNS----QCKAVTVLFLGILITLMTFSII-ELFIS 181
                                                                                                                                                                                                                           16;
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Best Local Similarity 28.0%; Pred. No. 2.9e-07;
Matches 45; Conservative 28; Mismatches 72; Indels
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                                                                              93 VLFINSGAFLIAVKRKTTETLIILSRIMNFLSALGAIAGIILL---
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nes 60; Conservative
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Best Local S:
Matches 60
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A;Cross-references: GB:X66187; NID:9396463; PIDN:CAA46955.1; PID:9396464
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A;Gene: Cj1040c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F1488.3 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 20.Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C; Cocession: T16070
R; Gelsel, C
Submitted to the EMBL Data Library, June 1995
A; Cocession: T16070
A; Reference number: 218456
A; Caesarion: T16070
A; Status: preliminary; translated from (B/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-455 <GET>
A; Residues: 1-455 <GET>
A; Experimental source: strain Bristol
C; Genetics:
C; Genetics:
A; Genetics:
A; Chara: 224/3; 289/2; 302/3; 370/2: 402/3, 242/3
A; Introns: 56/3; 193/2; 224/3; 289/2; 302/3; 370/2: 402/3, 242/3
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 16-7u1-1999 #sequence_revision 16-7u1-1999 #text_change 21-7u1-2000
C;Accession: JH0751
R;Bieber, T.; de la Salle, H.; Wollenberg, A.; Hakimi, J.; Chizzonite, R.; Ring, J.; Han J.; Exp. Med. 175, 1285-1290, 1992
A;Title: Human epidermal Langerhans cells express the high affinity receptor for immunog A;Reference number: JH0751; MUID:92235608
A;Accession: JH0751
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A;Molecule type: DNA
A;Residues: 1-307 <STO>
A;Cross-references: GB.AE005176; PID:q12724776; PIDN:AAK05853.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: ysbC
                                                                                                                                                                                                                                                                                                                                                                                                   72 IWIGGVL---GGIFL------TSNVLLFPR------LGAVQTVILPILGQILMGTLID 114
                                                                                                                                                                                                                                                                                                                                                                        91 ---GSVLFINSGAFLIAVKRKTTETLI‡LSRIMNFLSALGAIAGIILLTFGFILDQNYIC 147
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303 ILGLVEIYFGIISRRNLHLISLCINGISMCASGVLILFGLQKNYPTIYVLVFLIGY---A 359
                                                                                                                                                                                                                                                                             34 STOSPLOKLFARKMKILGTIQILFGIMTFSFGVIFL -- FTLLKPYPRFP-FIFLSGYPFW 90
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Genetics:
;Gene: CESP:F14BB.3
;Introns: 56/3; 193/2; 224/3; 289/2; 302/3; 370/2; 402/3; 442/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.0%; Score 103; DB 2; Length 455; llarity 31.6%; Pred No. 0.063; Conservative 15; Mismatches 32; Indels
                                                                                                                                                                                    Query Match 10.3%; Score 106; DB 2; Length 307; Best Local Similarity 31.9%; Pred. No. 0.023; Matches 46; Conservative 21; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 SVLFINSGAFLIAVKRKTTETLIILSRIMNFLSALGAI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 GYSHONSOCKAVTVL-FLGILITL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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A; Molecule type: DNA
A; Residues: 1-152 <BIE>
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Local S...
31;
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Best Local Si
Matches 31;
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probable inorganic phosphate transport protein PT1 - barrel medic
C:Species: Medicago truncatula (barrel medic)
C:Species: Medicago truncatula (barrel medic)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change.23-Mar-2001
C:Accession: T0782
R:Liu, H:; Trieu, A.T.: Blaylock, L.A.; Harrison, M.J.
Mol. Plant Microbe Interact: 11, 14-22, 1998
A;Title: Cloning and characterization of two phosphate transporters from Medicago tru
A;Accession: T07892
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Medicule type: mRMA
A;Mesidues: 1-537 <LIU>
A;Cross-references: EMBL:AF000354; NID:g2465526; PIDN:AAB81346.1; PID:g2465527
C:Genetics:
A;Gene: PT1
C;Superfamily: probable inorganic phosphate transport protein PHO84
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Cibate: 31-Mar-2000
Cibate: 31-Mar-2000
A:Pitle: The ganome sequence of the food-borne pathogen Campylobacter jejuni reveals A:Pitle: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals A:Accession: E81306
A:Pitle: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals A:Accession: E81306
A:Sterin: preliminary
A:Molecule type: DNA
A:Molecule type: DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable transmembrane transport protein Cj1040c [imported] - Campylobacter jejuni (s C;Species: Campylobacter jejuni C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
                                                                                                                                 3;
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                                                                                                                                                                                                                                        83 FLSGYPFWGSVLFINSGAFLIAVKRKTTETLIILSRIMNFLSALGAIAGIILLTFGFILD 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 LLKPYPRFPFI---FLSGYPFWGSVLFINSGAFLIAVKRKTTETLIILSRIMNFLSALGA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                      26 FKAGYPFWGAIFFSISGMLSIISERRNATYLVRGSLGANTASSIAGGTGITLL----IIN 81
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 FPPEITASEYESTELSATTFSTQSPLQKLFARKMKILGTIQI--LFGIMTFSFGVIFLFT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 FDKEFSTSMVLFAQLVAAPVSLFGPL--LLGKLRQNLHTFYIAGLCSMYVIAFGMLFIFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 QNYICGYSHQNS----QCKAVTVLFLGILITLMTF-SIIELFISLPFSILGCHSE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
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            Length 152;
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Query Match 9.7%; Score 100; DB 2; Length 15
Best Local Similarity 27.6%; Pred. No. 0.042;
Matches 32; Conservative 21; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 IAGIILLTFGFILDQNYICGYSH---QNSQCKAVTVLFLGILITLMTF 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65; Indels
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9.3%; Score 96; DB 2;
Best Local Similarity 25.0%; Pred. No. 0.24;
Matches 42; Conservative 31; Mismatches
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Vature 392, 353-358, 1998

A.Fitle: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A.Reference number: A70300; MUID:98196666
A.Rocession: C70379
A.Scatus: preliminary; nucleic acid sequence not shown; translation not shown
A.Rocelecule type: DNA
A.Rocesion: 1-408 <AQPS
A.Cross-references: GB:AE000713; NID:92983424; PIDN:AAC07022.1; PID:92983440; GB:AE00
A.Experimental source: strain VF5
A.Genetics:
A.Genetics:
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R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
A;Cross-references: GB:AE001227; GB:AE000520; NID:g3322797; PIDN:AAC65503.1; PID:g332
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein aq_917 - Aquifex aeolicus
C;Species; Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: C70379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSVLFINSGAFLIAVKRKTTETLIILSRIMN-----FLSALGAI-AGIILLT----- 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGFINLNHKYLFDLHMSFMLFGWTATLVASVSFQVIEMFFVTPPYPKFISSYLPKTVFTL 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 VI-FLETLLKPYPRFPFIFLSGYPFWG----SVLFINSGAFLIAVKRKTT------ 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 VLFVQSPIIHSDAYTSVILKQATLSTEEDPEQALWSVHTKNIWLLPNNQLAFSHGVLSFG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 QSPLOK-LFARKMKILGTIQILFGIMTFS----FGVIFLFTLLKPYPRFPFIFLSGYPFW 90
                                                                                                                                                                                                                                                                                                                                             10 VPLVFPPEITASEYESTELSATTFST-QSPLQKLFA---RKMKILGTIQILFGIMTFSFG 65
                                                                                                                                                                                                                                                                                     25;
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                                                                                                                                                                                                                           Length 991;
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                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58;
                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                       9.2%; Score 94.5; DB
28.3%; Pred. No. 0.81;
tive 21; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265 AQEEAPNYLKISADYSALGGMAGI 289
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                                                                                                                                                                                             Query Match
Best Local Similarity 28.3..,
Local 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52; Conservative
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Best Local Similarity
Matches 52; Conserva
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F9920B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: DNA
A,Residues: 1-165 <MTH>
A,Cross-references: GB.AE000859; GB:AE000666; NID:g2621902; PIDN:AAB85313.1; PID:g262190
A,Experimental source: strain Delta H
C;Genetics:
A,Gene: MTH813
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Conserved hypothetical protein TP0515 - syphilis spirochete
C; Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C; Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C; Accession: B71315
R; Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Fraser, C.M.; Norris, S.J.; Weinstock, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; Science 281, 375-388, 1998
A; Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A; Reference number: A71250; MUID: 98332770
A; Reference number: A71250; MUID: 98332770
A; Reference number: DNA
A; Molecule type: DNA
A; Residues: 1-991 <COL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 GSVLFINSGAFLIAVKRKTTETLIILSRIMNFLSALGA-IAGIILLTFGFILDQNYICGY 149
                                                                                                                                                                                                                                                                                                                                                          112 TLIILSRIMNF---LSALGAIAGIILLTFGFI------LDQNYICGYSHQNSQCKA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                    ----REPFIFLSGYPFWGSVLFINSGAFLIAVKRKTTE 111
                                                                                                                                                                                                                                                        377 MMGFFFMTVFMFGLAIPYDHWSKEENRIGFVVMYSLTFFFSNFGPNAATFVVPAE---- 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 KILGTIQILEGIMTESF ----- GVIFLETLIKPYPRFPETFLSGYPFW ---- 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 KIPGLISLILGILVILFPVFSVFTLSVLTGVAVLFVAI------WLFLLGSGTWKVNRG 63
                                                                                                                                            Gaps
                                                                                                                                      27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38;
                                                                              Length 537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 165; 0.13; thes 54; Indels
                                                                                                                                      50; Indels
                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.3%; Score 95; DB 7.25.3%; Pred. No. 0.13. ive 23; Mismatches
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August 27, 2002, 11:02:16; Search time 65.04 Seconds (without alignments) 341.555 Million cell updates/sec
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries A_Geneseq_032802:* 1: /SIDS1/qcqdata/ Database :

1: /SIDSJ/gcgdata/hold-geneseq/genesegp-embl/AA1980.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human CD20/IgE-rec Human secreted pro Novel human membra Human gene 9 encod Human reproductive Novel human membra Human secreted pro Novel human membra Novel human membra Human secreted pro
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% Query Match	100.0 100.0 97.8 91.2 91.2 71.6 66.9 56.7 28.6
Score	1027 1027 1027 1004 937 937 735.5 687 582 414 263.5
Result No.	11 10 10 11

High affinity immu Human high affinit	Human secreted pro	Human polypeptide,	Human inflammation				Dendritic cell (DC	Human hHAIERbs-iso	Human breast tumou	Lung cancer associ	Human secreted pro	Human secreted pro	Human protein sequ		n cell surf		HTm4 protein. Hom	Chandra, a helper	Novel human diagno	Human receptor pro	Novel human diagno	Dendritic cell (DC	Human CD20 antigen	Human secreted pro	CD20.4 antigen.	Human cell surface	Human lymphocyte c	Human HAIERbs isof	Extended human sec	Human HAIERbs isof	Human CD20 antigen	Human CD20.4 antig
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19.7	19.7	19.6	17.9	17.9	17.9	17.9	17.9	17.9	17.9	17.9	17.9	17.9	17.9	17.9	17.8	17.7	17.7	17.5	17.2	16.8	16.8	16.7	16.7	16.6	16.5	16.5	16.5	16.4	16.4	16.4	16.4	16.4
202.5	202.5	201.5	183.5	183.5	183.5	183.5	183.5	183.5	183.5	183.5	183.5	183.5	183.5	183.5	182.5	181.5	181.5	180	176.5	172.5	172.5	171	171	170.5	169	169	169	168	168	168	168	168
12															28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

06-MAR-2000; 2000US-0187470.

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The invention relates to human CD20/immunoglobulin E (IgE) receptor like polypeptides designated as agp-96614-al and agp-69406-al and nucleic acid molecules encoding such polypeptides. Polypeptides of the invention are useful for treating, preventing or ameliorating a disease, condition, or disorder which includes cancer such as brain cancer; abnormal cell proliferation such as arteumatoria arthritis, advormal cell proliferation such as arteumatoria arthritis, auchamine disease, multiple sclerosis, such as arteumatoria arthritis, auchamine diseases, multiple sclerosis, diabetes, transplant rejection and reproductive diseases such as infertility, preterm labour and delivery, endometriosis etc. They are also useful for identifying antagonists and as immunogens, for raising antibodies which may also be used to prevent, treat or calsances and diseases and disorders. Polynucleotides of the invention are used to map the location of CD20/IGE-receptor like gene and related genes on chromosomes and as hybridisation probes. They are also useful in gene therapy. The present sequence is human CD20/IGE-receptor like protein, agp-96614-al.
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              Novel CD20/IgE-receptor like polypeptides and polynucleotides, antagonists and antibodies of the polypeptide useful for treating ameliorating or preventing diseases associated with the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22; Length 200;
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100.0%; Pred. No. 2.9e-111;
ative 0; Mismatches 0;
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                                                                                                   Claim 13; Fig 1; 145pp; English.
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Best Local Similarity 100.0
Matches 200; Conservative
                                                                    e.g. cancer, asthma
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07-DEC-2000; 2000WO-IB01938.

WO200142451-A2.

14-JUN-2001

99US-0169629

08-DEC-1999;

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potentially secreted proteins. The nucleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosis of they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GENGET gene expression. For example, they be used to treat disorders associated with decreased GENGET gene expression by rectifying mutations or deletions in a patient's genome that affect the activity of GENSET or by supplementing the patients own production of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate GENSET expression by binding with the cells' own genes and preventing their expression. The sense and antisense nucleic acids may also be presence of similar nucleic acid sequences in samples, and hence to determine which patients may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and ansays to identify modulators (agonists and ansays to identify modulators (agonists) of GENSET polypeptide expression and activity. The present sequence is a GENSET polypeptide of the invention.
                                                                                                                                                 Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety of diseases, and for diagnosis of those diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 NFLSALGAIAGIILLTFGFILDQNYICGYSHQNSQCKAVTVLFLGILITLMTFSIIELFI 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to full length GENSET human nucleic acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; membrane receptor; IgE receptor; CD20;
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100.0%; Pred. No. 2.9e-111;
tive 0; Mismatches 0;
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                                                                     Bougueleret L,
                                                                                                                                                                                                                       Claim 21; Page 802-803; 921pp; English.
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ID AAU01210 standard; Protein; 199 AA.
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physiological disorder.
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Best Local Similarity
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N-PSDB; AAH64741.
                                  (GEST ) GENSET
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Gaps

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Human; immune system-related protein; allergy; rheumatoid arthritis; cancer; Gaucher's disease, Viral hepatitis; gene therapy; cytostatic; diabetes mellitus; arrhythmia; wound healing; ischaemic lesion; AlDS; Acquired Immune Deficiency Syndrome; virucide; hepatotropic; vasotropic; autoimmune disorder; inflammation; cardiovascular disorder; hair loss; wound healing; cell proliferation; skin aging; endocrine disorder; food preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated immune system-related polypeptide useful for treating
                                                                                                                                                                       /label= Immunogenic_epitope
                                                                                                                                                                                               /label= Immunogenic_epitope
                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  Hilbert D, Kenny JJ, Moor
JR, Endress GA, Ruben SM;
                                                                                                                                                                                                                                                                                                                11-AUG-2000; 2000US-224367P.
                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                            07-MAR-2001; 2001WO-US07260.
                                                                                                                                                                                                                                                                                                     08-MAR-2000; 2000US-187873P
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                                                                                                                                                                                                                                                 Polynucleotide encoding novel human membrane protein, useful for identifying agonist, antagonist or modifiers or for producing antibodies useful in therapeutic, diagnostic and pharmacogenomic
                                                                                                                                                                                                                                                                                                                                          present sequence represents novel human membrane protein #1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human gene 9 encoded immune system-related protein HTENN45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
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Pred. No. 1.4e-108;
); Mismatches 2;
                             /note= "Encoded by TGTTGT"
Location/Qualifiers
199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE10917 standard; Protein; 201 AA.
                                                                                                                                                                                                                                                                                                                 Claim 2; Page 29-30; 32pp; English.
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0
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                                                                                                                                                          (LEXI-) LEXICON GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.8%;
99.0%;
                                                                                                                                 99US-0171567.
                                                                                                         2000WO-US33742.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 99.0
Matches 197; Conservative
                                                                                                                                                                                    Turner CA;
                                                                                                                                                                                                            WPI; 2001-408646/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199 AA;
                                                                                                                                                                                                                           N-PSDB; AAS04279.
                 Misc-difference
                                                       WO200146417-A2
                                                                                                       12-DEC-2000;
                                                                                                                                                                                                                                                                                           applications
                                                                                                                                 22-DEC-1999;
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                                                                                28-JUN-2001
                                                                                                                                                                                    Walke DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE10917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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ID AAE11
XX
AC AAE1
XX
DT 18-D
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DE Huma
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Ebner R;

Soppet DR,

Moore PA, Choi GH,

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                                                                                                                                                                                                                                                                   DNA. Human immune-system related protein and DNA are useful for preventing, treating or ameliorating a medical condition in a mammalian subject, for diagnosing, preventing or treating immune system-associated disorders, autoimmune disorders (rheumatoid arthritis), inflammatory disorders (allergies), immunodeficiencies (AIDS), inflammatory disorders (allergies), infectious diseases (e.g., viral hepatitis), complement activation disorders, immune complex diseases, neoplastic disorders (cancer), hyperproliferative disorders (Gaucher's disease), disorders cardiovascular disorders (arthritis), wound healing and epithelial cell proliferation, endocrine disorders (diabetes mellitus) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurological disorders (ischaemic lesions). Immune-system related protein or DNA is useful for preventing hair loss, skin aging due to sunburn, to maintain organs before transplantation, to treat weight disorders, to modulate mammalian characteristics, to change a mammal's mental or physical state, or as a food additive or preservative. Immune-system related DNA is useful in gene therapy, for chromosome identification, radiation hybrid mapping, long range restriction mapping and in forensic biolog. The present sequence represents a human immune-system related protein of the invention.
                                                                                                                                                                                                                                          invention relates to human immune system-related protein and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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rheumatoid arthritis, AIDS, allergy, cancer, Gaucher's disease, diabetes mellitus, arrhythmia, wound healing, ischemic lesions and
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Pred. No. 8.8e-101;
0; Mismatches 1;
                                                                                                                                                         Claim 11; Page 310-311; 315pp; English.
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99.5%;
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Best Local Similarity 99.5
Matches 187; Conservative
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2000US-0229345.
2000US-0229509.
2000US-0229513.
                                     2000US-0230437.
2000US-0230438.
2000US-0231242.
                                                                         2000US-0231244.
2000US-0231413.
2000US-0231414.
                                                                                                   2000US-0232080.
2000US-0232081.
2000US-0231968.
2000US-0232397.
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20000S-0233063
20000S-0233063
20000S-0233065
20000S-023423
20000S-023423
20000S-023499
20000S-0235484
20000S-0235834
                                                                                                                                       2000US-0232398.
2000US-0232399.
2000US-0232400.
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2000US-0241809
2000US-0244617
2000US-0246474
2000US-0246475
2000US-0246475
2000US-0246477
2000US-0246528
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2000US-0237039.
2000US-0237040.
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2000US-0249212.
2000US-0249213.
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2000US-0236327
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2000US-0236802
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2000US-0239937
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2000US-0241785
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2000US-0241787
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01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
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14-SEP-2000;
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13-OCT-2000;
13-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
08-NOV-2000;
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14 - SEP - 2000;
14 - SEP - 2000;
14 - SEP - 2000;
21 - SEP - 2000;
25 - SEP - 2000;
25 - SEP - 2000;
26 - SEP - 2000;
27 - SEP - 2000;
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29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
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29-SEP-2000;
29-SEP-2000;
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17-NOV-2000;
Human; reproductive system related antigen; reproductive system disorder;
cancer; gene therapy.
      antigen SEQ ID NO: 3772
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                                                                                                                                                                                                   Human reproductive system related
                                                                                                                                            AAM95114 standard; Protein; 212
                                                                                                                                                                                                                                                                                                                    20000S-0179065.
20000S-0180628.
20000S-0184664.
20000S-0186350.
2000US-0189874.
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2000US-0198123.
2000US-0205515.
2000US-0209467.
2000US-0214886.
2000US-021486.
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2000US-0217487.
2000US-0218290.
2000US-022828.
2000US-022864.
2000US-0224519.
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2000US-0225267.
2000US-0225268.
2000US-0225268.
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2000US-0225757.
2000US-0225758.
2000US-0226279.
2000US-0226681.
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2000US-0229343
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|slpfsiwg 188
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18 - AAF - 2000)
19 - AAF - 2000)
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30 - JUL - 2000)
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16 - AUG - 2000)
17 - AUG - 2000)
18 - AUG - 2000)
19 - AUG - 2000)
10 - SEP - 2000)
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24-FEB-2000;
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16-MAR-2000;
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08-DEC-2000;

06-DEC-2000; 08-DEC-2000 08-DEC-2000; 08-DEC-2000;

17-NOV-2000; 17-NOV-2000;

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Human membrane protein #4 is 1 of 4 human membrane proteins the protein membrane protein in the present invention. These membrane proteins share structural similarity with membrane receptors such as the igs receptor and mammalian CD20. The novel human membrane proteins are useful for identifying agonists, antagonists and medulators of the membrane proteins and proteins are useful for producing antibodies specific to the membrane proteins. The membrane proteins can be used for diagnosis, drug screening, pharmacogenomic applications, clinical trial monitoring and the treatment of physiological disorders and diseases. The polynucleotides encoding the membrane proteins can be used to generate per proteins or probes to identify mutations associated with a particular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TFSFGVIFLFTLLKPYPRFPFIFLSGYPFWGSVLFINSGAFLIAVKRKTTETLIILSRIM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 NFLSALGAIAGIILLFFGFILDQNYICGYSHQNSQCKAVTVLFLGILITLMTFSIIELFI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MDSSTAHSPVFLVFPPEITASEYESTELSATTFSTQSPLQKLFARKMKILGTIQILFGIM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polynucleotide encoding novel human membrane protein, useful for identifying agonist, antagonist or modifiers or for producing antibodies useful in therapeutic, diagnostic and pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence represents novel human membrane protein #4.
                                                                     Human; membrane protein; membrane receptor; IgE receptor; CD20;
physiological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 735.5; DB 22; Length 149;
Pred. No. 1.7e-77;
0; Mismatches 0; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB12234 standard; peptide; 158 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 31; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.68;
74.58;
                               Novel human membrane protein
                                                                                                                                                                                                                                                                                                       (LEXI-) LEXICON GENETICS INC
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26-SEP-2001 (first entry)
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Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                             Walke DW, Turner CA;
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-408646/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 AA;
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                                                                                                                                                             WO200146417-A2.
                                                                                                                                                                                                                                                                      22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         applications
                                                                                                                         Homo sapiens
                                                                                                                                                                                              28-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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ABB12234
ID ABB13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TFSFGVIFLFTLLKPYPRFPFIFLSGYPFWGSVLFINSGAFLIAVKRKTTETLIILSRIM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 NFLSALGAIAGIILLTFGFILDQNYICGYSHQNSQCKAVTVLFLGILITLMTFSIIELFI 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 91.2%; Score 937; DB 22; Best Local Similarity 99.5%; Pred. No. 9.4e-101; Matches 187; Conservative 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruben SM;
                                                                                                                                                                                                                                2000US-0250391.
2000US-0251030.
2000US-0251988.
2000US-0256719.
2000US-0251479.
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2000US-0249297.
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                                              17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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-DEC-2000;
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01-DEC-2000;
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Sequence

AAU01213

AAU01213 ID AAU0 XX AC AAU0 XX

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51; Gaps

ABB12234;

11-JAN-2002 (first entry)

Human secreted protein homologue, SEQ ID NO:2604.

Human; cytokine; cell proliferation; cell differentiation; growth factor; hemematopolesis requiation; tissue growth, immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoletic disorder; meyloid cell disorder; asthma; asthma; arthritis; chronic inflammatcry condition; proliferative retinopathy; chronic inflammatcry condition; proliferative retinopathy; bone disorder; osteoporosis; vascular growth disorder; osteoporosis; vascular growth disorder; chissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gehe therapy; antiinflammatory; antiastmatic; antiartiic; haemostatic; antiarteriosclerotic; cytostetic; osteopathic; vascitopic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer;

Homo sapiens.

WO200157188-A2.

09-AUG-2001.

05-FEB-2001; 2001WO-US03800.

03-FEB-2000; 2000US-0496914. 27-APR-2000; 2000US-0560875.

HYSE-) HYSEQ INC.

Tang YT, Liu C, Drmanac RT;

WPI; 2001-457740/49. N-PSDB; ABA09478. Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammallan subject e.g. arthritis and cancer -

Claim 20; Page 318; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABB10981-ABB12330 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the larvention, methods of producing the novel polypeptides, and hence polypeptides, methods of detecting the nucleotides, cor polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention have homology to known proteins, thereby of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may differentiation activities; stem for activity; state growth activity; differentiation activities; stem for activity; the propable activities; haematopoiesis regulatory activity; tissue growth activity; chanced activities; heamatopoiesis receptor or inhibin-related activities; chemotatic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, and nucleotides of the invention are useful for preventing, treating or metastasis.

Conditions, e.g., by protein or gene therapy, Such conditions include cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), arterial ischaemia, bone disorders (e.g., myeloid or lymphoid cell disorders, carcers, haematopoletic disorders (e.g., myeloid or lymphoid cell disorders (e.g., myeloid or lymphoid cell cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell disorders (e.g., myeloid or lymphoid cell cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell disorders (e.g., myeloid or lymphoid cell cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell ceptor or setting or gene therapy. Such conditions (e.g., by broaden or gene therapy such myeloid or lymphoid or

ö Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides screening techniques. The present sequence represents a novel human polypeptide of the invention. The present sequence represents novel human membrane protein #3. Human membrane protein #3. Human membrane proteins #3 is 1 of 4 human membrane proteins (AAU01210-AAU01213) given in the present invention. These membrane proteins share structural similarity with membrane receptors such as the 1gE receptor and mammalian CD20. The novel human membrane proteins are useful for identifying agonists, antagonists and modulators of the membrane proteins, and for producing antibodies specific to the Gaps 1 MDSSTAHSPVFLVFPPEITASEYESTELSATTFSTQSPLQKLFARKMKILGTIQILFGIM 60 Polynucleotide encoding novel human membrane protein, useful for identifying agonist, antagonist or modifiers or for producing antibodies useful in therapeutic, diagnostic and pharmacogenomic ö Human; membrane protein; membrane receptor; IgE receptor; CD20; Length 158; 1; Indels DB 22; Score 687; DB 22 Pred. No. 8e-72; 0; Mismatches Disclosure; Page 30-31; 32pp; English. AAU01212 standard; Protein; 138 AA. Novel human membrane protein #3. 121 NFLSALGAIAGIILLTFGF 139 Query Match
Best Local Similarity 99.3%;
Matches 138; Conservative (LEXI-) LEXICON GENETICS INC 99US-0171567. 12-DEC-2000; 2000WO-US33742. (first entry) physiological disorder. Turner CA; 2001-408646/43. 158 AA; N-PSDB; AAS04281 WO200146417-A2. Homo sapiens. 22-DEC-1999; applications 26-SEP-2001 28-JUN-2001. Walke DW, Sequence AAU01212; AAU01212 8888888888 g g ğ ò δ q

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membrane proteins. The membrane proteins can be used for diagnosis, drug screening, pharmacogenomic applications, clinical trial monitoring and the treatment of physiological disorders and diseases. The polynucleotides encoding the membrane proteins can be used to generate proximers or probes to identify mutations associated with a particular
                                                                                                                                                                                                                                                                                         1 MDSSTAHSPVFLVFPPEITASEYESTELSATTFSTQSPLQKLFARKMKILGTIQILFGIM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotide encoding novel human membrane protein, useful for identifying agonist, antagonist or modifiers or for producing antibodies useful in therapeutic, diagnostic and pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     membrane protein; membrane receptor; IgE receptor; CD20;
                                                                                                                                                                                               9
                                                                                                                                                               Length 138;
                                                                                                                                                                                                 Indels
                                                                                                                                                               Query Match 56.7%; Score 582; DB 22; Best Local Similarity 92.1%; Pred. No. 1.1e-59; Matches 117; Conservative 4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 30; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU01211 standard; Protein; 81 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human membrane protein #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      physiological disorder
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N-PSDB; AAS04280.
                                                                                                                      138 AA;
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|121 iltkivs 127
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                                                                                                                        Sequence
                                                                                         disease.
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and the treatment of physiological disorders and diseases. The polynucleotides encoding the membrane proteins can be used to generate PCR primers or probes to identify mutations associated with a particular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' unts is rarely included. 5' ESTs are derived from mRNAs with intext 5' UTR is rarely procedure be used to obtain full length cDNAs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                         New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
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                                                                                                                                Length 81;
                                                                                                                                                                Indels
                                                                                                                                   DB 22;
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                                                                                                                                 Score 414; DB 22
Pred. No. 2e-40;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted protein, SEQ ID NO: 7155.
                                                                                                                                                                                                                                                                                                                                                                        AAG03074 standard; Protein; 77 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                              180 ISLPFSILGCHSEDCDCEQCC 200
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                                                                                                                                40.3%;
ilarity 97.5%;
Conservative
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N-PSDB; AAC03080.
                                                                                                                                                  Local Similarity
nes 79; Conserv
                                                                                     81 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEST ) GENSET.
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                                                                                         Sequence
                                                                                                                                   Query Match
                                                          disease
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Length 67;

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                                                                                                                                                                                                                                                                                                                                                                                Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
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                                              Gaps
                                                                         FSTQSPLQKLFARKMKILGTIQILFGIMTESFGVIFLFTLLKPYPRFPFIFLSGYPFWGS 92
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0
           Length 77;
                                              Indels
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           Score 294; DB 21;
Pred. No. 1.7e-26;
3; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                 Human secreted protein, SEQ ID NO: 262.
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                                                                                                                                                                                                                                                   AAG89142 standard; Protein; 67 AA
           28.6%;
83.6%;
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06-MAR-2000; 2000US-0187470.
                                                                                                                                                                                                                                                                                                                  (first entry)
Query Match
Best Local Similarity 83.69
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N-PSDB; AAH64745.
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                                                                                                                                                       93 VLFINSG 99
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                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                  11-SEP-2001
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                                                                                                                                                                                                                                                                                    AAG89142;
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High affinity immunoglobulin E receptor-like protein; IGERB; Incyte clone 927955; inflammatory response; AIDS; Addisons's disease; atherosclerosis; bronchitis; ulcerative collitis; diabetes mellitus; emphysema; gout; Garves's disease; osteoporosis; rheumatoid arthritis; Sjogren's syndrome; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a high affinity immunoglobulin E receptor-like protein (IGERB). The present sequence was first identified in Incyte clone 927955 for the brain cDNA library BRAINOTO4. POLYNUCleotides complementary to the IGERB CONA can be used as probes to IGERB gene expression. IGERB proteins and nucleotides may be used for the diagnosis of inflammatory responses associated with expression of IGERB, e.g. AIDS, Addisons's disease, atherosclerosis, bronchitis, ulcerative colitis, diabetes mellitus, emphysema, gout, Garves's disease, osteoporosis, rheumatoid arthritis, Sjogren's syndrome and complications of cancer. The sequences may also be useful in assays that detect activation or
                                    Gaps
                                                                 1 MDSSTAHSPVFLVFPPEITASEYESTELSATTFSTQSPLQKLFARKMKILGTIQILFGIM 60
                                                                                                54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "potential protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "potential casein kinase II phosphorylation
site"
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                                                                                    9.
                                                                                                                                                                                                                                                                                                                                             High affinity immunoglobulin E receptor-like protein (IGERB).
Score 263.5; DB 22; Length
Pred. No. 5.1e-23;
3; Mismatches 7; Indels
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192
/note= "potential casein kinase II phos
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                                                                                                                                                                                                                                              AAW96745 standard; Protein; 239 AA.
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                                                                                                                                                                                                                                                                                                              (first entry)
 Query Match
Best Local Similarity 74.7
Matches 56; Conservative
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                                                                                                                                 61 TESFGVIFLFTLLKP 75
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Modified-site
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17-AGG-1998;
04-SEP-1998;
23-OCT-1998;
08-JAN-1999;
12-FEB-1999;
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                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                           IGERB; high affinity; immunoglobulin E; IgE; receptor; allergy; inflammation; B lymphocyte; homology; high affinity IgE receptor; FCRI; mast cell; basophil; histamine; protease; cytoplasmic granule; synthesis; effector; prostaglandin; leukotriene; cytokine; antigen; antibody; identification; agonist; antagonists; expression; activity; diagnosis; therapy; inflammatory disorder; multiple sclerosis; osteoarthritis; asthma; cancer; side effect; complication.
                                                                                            SGAFLIAVKRKTTETLIILSRIMNFLSALGAIAGIILLIF--GFILDQNYICGYSHQNSQ 155
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents human high affinity immunoglobulin E (IgE) receptor-like protein (IGERB). Nucleic acids encoding IGERB were initially identified in a brain cDNA library, this sequence being a
                                                                               LQKLFAR-KMKILGTIQILFGIMTFSFGVIFLFTLLKPYPRFPFIFLSGYPFWGSVLFIN 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High affinity immunoglobulin E receptor-like protein useful for stimulating allergic and immune responses -
                                                              3;
                                           Length 239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Phosphorylated by casein kinase II"
                                                                                                                                                                                                                                                                                                                                                                                                          by protein kinase
                                                              71; Indels
                                                                                                                                                                                                                                                                            Human high affinity IgE receptor-like protein (IGERB).
                                           DB 20;
                                            Score 202.5; DB 2
Pred. No. 3.2e-15;
                                                                                                                                                                  CKAVTVLFLGILITLMTFSIIELFISLPFSILGC 189
                                                              31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Phosphorylated
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 induction of various cancers.
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                                             19.7%;
ilarity 31.8%;
Conservative 3
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                                                       Similarity
                    239 AA;
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Modified-site
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                                                                 49;
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                    Sequence
                                              Query Match
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consensus. An allergic response is initiated by release of IgE from B Lymphocytes. The IgE molecules then bind to the high affinity (from B Lymphocytes. The IgE molecules then bind to the high affinity concludes of histamine and proteases from cytoplasmic granules and the release of histamine and proteases from cytoplasmic granules and cade to the synthesis of effectors of the allergic and inflammatory leads to the synthesis of effectors of the allergic and inflammatory concepts. It may be administered to stimulate allergic and inflammatory and inflammatory and inflammatory and inflammatory and allergic and inflammatory and antipodies and to identify concepts and antagonists of IGERB expression and activity. The antibodies may also be used in diagnosis. Antibodies and antagonists may be administered to downregulate IGERB activity and reduce the potency of inflammatory and allergic responses. They may be used in this way to treat inflammatory disorders such as multiple sclerosis, cateoarthritis, asthma and some complications of cancer. Conversely, the gonists may be used to enhance immune responses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 SGAFLIAVKRKTTETLIILSRIMNFLSALGAIAGIILLTF--GFILDQNYICGYSHQNSQ 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 LOKLFAR-KMKILGTIQILFGIMTFSFGVIFLFTLLKPYPRFPFIFLSGYPFWGSVLFIN 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 CKAVTVLFLGILITLMTFSIIELFISLPFSILGC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ::|:::|||174 chgtmsilmgldgmvlllsvlefciavslsafgc 207
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98US-0099229.
98US-0105368.
99US-0115234.
99US-0119931.
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es 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 AA;
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Search completed: August 27, 2002, 11:04:05 Job time: 109 sec
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                                                                                                                                                                                                                                                                                           ANY9489 to AAY94980, isolated from human settled process. Since AAY94989 to AAY94980, isolated from human adult brain, adult thyroid, adult retina, foetal carcinoma, adult blood, adult neural, foetal kidney, adult placenta, adult testis, whole embryo, adult cartilage, kidney, foetal brain, adult thymus, foetal placenta, adult uterus, adult tumour, and adult bladder, cDNA libraries. The polynucleotides and proteins are predicted to have blological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. The polynucleotides can be used as markers for tissues in which the protein is preferentially expressed, as molecular weight markers on Southern gels, and as Chromosome markers or to map gene posticions. The proteins can be used in the treatment of immune deficiencies and disorders, such as severe combined immunedeficiency (SCID), as well as viral, bacterial, fungal and other infections. These infections include human immunodeficiency virus (HIV), hepatitis, herpesviruses, mycobacteria, Leisamania spp., malaria and candidasis. The proteins can be lused to treat autoimmune disorders such as connective tissue disease, multiple sclerosis, systemic lupus crythematosis, rheumatoid arthritis, leisamania spp., malaria and candidasis, rheumatoid arthritis, autoimmune pulmonary inflammation, cullialah-Barre syndrome, autoimmune theory or probes for the human secreted proteins can also be used to treat allergic conditions, such asthma. AAA16698 to AAA16774 represent proteins.
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                                                                                                                                                                              have e.g.
                                                                                                      <u>``</u>
                                                                                                                                                                                                                                                                                  to AAA16697 encode the human secreted proteins given in
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                                                                                       Collins-Racie LA, Evans C;
Steininger RJ, Spaulding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.7%; Score 202.5; DB 21; Length 245; 31.8%; Pred. No. 3.4e-15;
                                                                                                                                                                            New polynucleotides encoding secreted proteins, which may inutritional, chemokine, immune stimulating or suppressing, hematopolesis regulating, tissue growth, activin/inhibin antiinflammatory or tumor inhibition activity
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3.4e-15; 71;
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                                                                                     LaVallie ER, C
1, Agostino MJ,
Fechtel K;
                                                                                                                                                                                                                                                       Claim 161; Page 607; 641pp; English.
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99US-0120575.
99US-0132020.
99US-0096622.
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                                                          (GEMY ) GENETICS INST INC.
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                                                                                     K, MCCOY JM, L
D, Treacy M,
, Clark HF, Fe
                                                                                                                                              WPI; 2000-205979/18
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18-FEB-1999;
30-APR-1999;
11-AUG-1999;
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Best Local Si
Matches 49,
                                                                                       Jacobs K,
                                                                                                     Merberg D
Wong GG,
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been clones. 830 cDNA molecules sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Finances for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA assity without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primers useful for synthesizing full length cDNA clones and their in genetic manipulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 220;
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Human; full length cDNA; cDNA synthesis; oligo-capping.
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                                                                                                                                                                                                                                                                                                                  99JP-0194486.
2000JP-0118774.
2000JP-0183765.
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Best Local Similarity 31.8%
Matches 49; Conservative
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                                                                                                                                                                                                                                                                                                                                                11-JAN-2000;
02-MAY-2000;
                                                                Homo sapiens
                                                                                                                          EP1130094-A2
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SEQUENCE CHARACTERISTICS:
LENGTH: 1669 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; IMMEDIATE SOURCE:
; LIBRARY: BRAINOTO4
; CLONE: 927955
US-08-916-902A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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3802.066 Million cell updates/sec
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1, Appl
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                                                                                                                       Search time 49.1 Seconds
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-318-492-3
US-08-707-340-3
US-08-707-340-3
US-08-703-463-22
US-09-103-463-14
US-08-379-482A-2
US-09-38-982-327
US-09-38-982-327
US-08-184-632-1
US-08-691-641-4
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US-08-65-1
US-08-461-809-9
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US - 08 - 924 - 747 - 25
US - 09 - 247 - 373B - 25
US - 09 - 296 - 715 - 25
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US-09-340-993-12
US-09-468-442-12
US-09-797-906-3
                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                 383533 seqs, 122816752 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                   nucleic search, using sw model
                                                                                                                       August 30, 2002, 00:43:57
                                                                                                                                                                                                                                                                                         IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                    Sequence
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APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HIGH AFFINITY IMMUNOGLOBULIN E
TITLE OF INVENTION: RECEPTOR-LIKE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
US-09-387-574-11
US-09-68-096-11
US-07-593-657-14
US-08-313-681A-3
US-08-322-911-3
US-08-021-608D-9
US-08-726-160-9
US-08-726-160-9
US-08-726-160-1
US-08-726-160-1
US-08-726-119-12
US-09-232-191-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/916,902A FILING DATE: Herewith CLASSIFICATION: 536 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE: ATORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0371 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08916902A
Patent No. 5871930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
  1359
1359
319
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2381
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Gaps

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Length 1669;

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Patent No. 552332

GENERAL INFORMATION:

APPLICANT: Lain, Bing
APPLICANT: Leilas, Jean-Michel
TITLE OF INVENTION: RECOMBINANT HTM4 GENE, PROTEIN AND
TITLE OF INVENTION: ASSAYS

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: AMBILTON, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                               Score 86.4; DB 2; Length 1 Pred. No. 3.4e-13; 0; Mismatches 216; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  630 tattcatttctctgcctttctcaattttggggtg 663
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                    5:
                                  INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1669 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                 Query Match 11.4%;
Best Local Similarity 51.1%;
Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Two Militia Dr
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173
      415-845-4166
                                                                                                                    IMMEDIATE SOURCE:
LIBRARY: BRAINOTO4
CLONE: 927955
                                                                                                                                                                                         ; CLONE; 9
US-09-213-389-2
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      Length 1669;
11.4%; Score 86.4; DB 2; Length 151.1%; Pred. No. 3.4e-13; ive 0; Mismatches 216; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09213389
Sequence 2, Application US/09213389
Fater No. 597072
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HIGH AFFINITY IMMUNOGLOBULIN E
TITLE OF INVENTION: RECEPTOR-LIKE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/916,902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Billings, Lucy J. RECIGYRATION WUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                      Matches 232; Conservative
  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-09-213-389-2
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Pred. No. 7.1e-07;
0; Mismatches 214; Indels
                                                                                                                                                                                                                                                             Patentin Release #1.0, Version #1.30
                    Smith & Reynolds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: B.H94-03A2
REFERENUICATION INFORMATION:
TELECPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1661 base pairs
                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Ver.
SOFTWARR: Patentin Release #1.0, Ver.
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/707,340
FLING DATE: 03-SEP-1966
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/318,492
FILING DATE: 06-CCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/675,648
FILING DATE: 03-UL-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYOOK, DAVID E.
REGISTRATION NUMBER: 22,520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 8.1%;
Best Local Similarity 50.6%;
Matches 238; Conservative
                                             Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                      ADDRESSEE: Hamilton,
STREET: Two Militia I
CITY: Lexington
STATE: Massachusetts
CORRESPONDENCE ADDRESS:
                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                        STATE: Massachus
COUNTRY: U.S.A.
ZIP: 02173
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8.1%; Score 61.6; DB 1; Length 16

Best Local Similarity 50.6%; Pred. No. 7.1e-07;

Matches 238; Conservative 0; Mismatches 214; Indels
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Patent No. 5705615
GENERAL INPORMATION:
APPLICANT: Lim, Bing
APPLICANT: Adra, Chaker N.
APPLICANT: Lelias, Jean-Wichel
TITLE OF INVENTION: RECOMBINANT HTM4 GENE, PROTEIN AND
TITLE OF INVENTION: ASSAYS
NUMBER OF SEQUENCES: 4
     PatentIn Release #1.0, Version #1.25
                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,492
FILIND DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: BROOK, DAVId E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: BIH94-03
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 1661 base pairs
TYPE: NUCLELC acid
TYPE: NUCLELC acid
                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
US-08-318-492-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-707-340-3
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Gaps

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343 atttettteaggatateeattetggggetetgttttgtteattaattetggageetteet 402
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22, Application US/07869933; Patent No. 5770396
GENERAL INFORMATION:
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46..54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46..786
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LOCATION:
FEATURE:
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Best Local Similarity 50.6%; Pred. No. 7.1e-07;
Matches 23%; Conservative 0; Mismatches 214; Indels 18; Gaps
                                   654 CGTAACTATCTCTACCATAGCCATGTGTGCAATGCAAACTGCTGTAATT 703
              634 catttototgootttotoaattttggggtgooaotoagaggattgtgatt 683
                                                                                                                  Sequence 3, Application US/08994578
Patent No. 597268
GENERAL INFORMATION:
APPLICANT: Lim, Bing
APPLICANT: Adra, Chaker N.
APPLICANT: Lelias, Jean-Michel
TITLE OF INVENTION: HTM4 METHODS
OF TREATMENT AND ASSAYS,
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                           NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: B1994-03A2Z
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (781) 861-6240
TELEPRONE: (781) 861-9540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1661 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                         Lexington
Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 97..738
US-08-994-578-3
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                                                                                                     US-08-994-578-3
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APPLICANT: KINET, Jean-Pierre
TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
TITLE OF INVENTION: IMMUNGLOBULIN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
414 TGTTGTAGCAGGGATAAACCCACAAGAACATGGATACAGAACAGTTTTGGAATGAACAT 473
                                                                                                                                                                                                                                                                                                                                                                                                                            522
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STATE: VBA

ZIP: 22313-029
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/07/869,933
FILING DATE: 19920416
CLASSIETCATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT. Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/154 NIHD
TELECOMMUNICATION INFORMATION:
TELEFAN: (703)863-4109
TELEFAN: (703)863-4109
TELEFAN: (703)863-4109
TELEFAN: CASEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: SLESS ARE PASSING
LENGTH: ARE PASSING
LENGTH: SLESS ARE PASSING
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Gaps
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                                                                                                                etgittigitcaitaaiteiggageetteetaaitgeagigaaaagaaaaaceacagaaa 431
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248 aagttetggttggtttgatatgeetttgttttggaacagttgtetgetecacacatecaga 307
                                                                             308 cttcagactttgacgacgaagtgcttttattatatagagcaggctacccattctggggtg 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS' SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/232,463 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 5.8%; Score 44.2; DB 1;
Best Local Similarity 6.8%; Pred. No. 0.031;
Matches 28; Conservative 204; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-A04-1991
ATORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STRANDEDNESS: single
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APPLICANT: Kinet et al.
TITLE OF INVENTION: Isolation, characterization, and use of the human beta TITLE OF INVENTION: Isolation, characterization, and use of the human beta TITLE OF INVENTION: immunoglobulin E.
TITLE OF INVENTION: immunoglobulin E.
FILE REFERENCE: 50490
CURRENT APPLICATION NUMBER: US/09/103,663D
EARLIER APPLICATION NUMBER: 07/869,933
EARLIER FILING DATE: 1992-04-16
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
LENGTH: 2545
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                                                                                                                                                                                                                                                                                                                                                                              308 CTTCAGACTTTGACGACGAGGCCTTTTATTATAGAGCAGGCTACCCATTCTGGGGTG 367
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                                                                                                 Score 50.8; DB 1; Length 2545;
Pred. No. 0.00046;
0; Mismatches 137; Indels 6
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6.7%; Score 50.8; DB 4;
Best Local Similarity 52.6%; Pred. No. 0.00046;
Matches 159; Conservative 0; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22, Application US/09103663D Patent No. 6171803
                                                                                                   Query Match 6.7%;
Best Local Similarity 52.6%;
Matches 159; Conservative
      mat_peptide
55..786
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LOCATION: (46)..(54)
FEATURE:
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US-09-103-663-22
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    ; NAME/KEY:
; LOCATION:
US-07-869-933-22
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                   126 tgtttctggtatttcctccagaaatca¢tgcttcagaatatgagtccacagaactttcag 185
                                                                                                                                                                                                   246 tagggactatccagatcctgtttggaattatgaccttttcttttggagttatcttccttt 305
 tcatctcctttcaaattatcaccgaca¢catcatggattcaagcaccgcacagtccgg 125
                                                                                                                                    ccacgaccttttcaactcaaagccccttgcaaaaattatttgctagaaaatgaaaatct 245
                                                                                                                                                                                                                                                                    306 tcactttgttaaaaccatatccaaggt\psitccctttatattttctttcaggatatccattct 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Brugilera, Filippa
APPLICANT: Holton, Timothy A
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING
TITLE OF INVENTION: GLYCOSYLTRANSFERASE ENZYMES AND USES THEREFOR
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                     366 ggggctctgttttgttcattaattctggagccttcctaattgcagtgaaaagaaaacca
                                                                                                                                                                                                                                                                                                                                                                                                                                     1454 CITTAACTACTIGCATAGATAGGIAATTACAGIGAIGCCTACATGCCGT 1502
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ZIP: 11530

COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379, 482A
FILING DATE: 30-JUL-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAMME: Didigilo, Frank S:
REGISTRATION NUMBER: 9590
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516)742-4346
TELEERA: (516)742-4366
TELEEX: 239 901 SANS UR
INFORMATION POR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Scully, Scott, Murphy & Presser
400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08379482A Patent No. 5859334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Garden City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1..1413
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                                                                                                                                                                                                1529 GAATGTGGCTGTAAAATGCTACTATTTGATTGTCAGATAAGGTCACATTTCATTACTTCT 1588
                                                                                                                                                                      651 caattttggggtgccactcagaggattgtgattgtgaacaatgttgttgactagcactgt 710
                                                                                   Sequence 1, Application US/08648298
Patent No. 5871990
GENERAL INFORMATION:
APPLICANT: Henrik Clausen
APPLICANT: Eric Paul Bennett
TITLE OF INVENTION: UDF-N-acetyl-alpha-D-galactosamine:polypeptide
TITLE OF INVENTION: N-acetyl-alpha-D-galactosamine:polypeptide
TITLE OF SEQUENCES: 19
        Length 1738;
                                                                                                                                                                                                                                                                               Sequence 327, Application US/09385982

Fatent No. 626234

GENERAL INFORMATION:
FALL OF INVENTION:
TITLE OF INVENTION: NOVEL HUMAN GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS:
CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1999-01-27
SEARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
SEARLIER FILING DATE: 1999-01-27
SEARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 658;
    Score 42.4; DB 2; Length 1
Pred. No. 0.055;
0; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
5.4%; Score 41; DB 4;
Best Local Similarity 71.6%; Pred. No. 0.092;
Matches 53; Conservative 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: n = A,T,C OF G
US-09-385-982-327
    ch 5.6%;
1 Similarity 57.1%;
97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  747 aaaaaaaaaaaa 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                  US-09-385-982-327/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 327
LENGTH: 658
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US-08-648-298-1
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1767 AAGTTTGGAGCACTAGTTTGATTATTATGTTTATTACAATTTTTAATAAATTGAATAGGT 1826
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APPLICANT: McCoy, John
APPLICANT: LaVallie, Edward
APPLICANT: Racie, List
APPLICANT: Racie, Lava
APPLICANT: Racie, Lava
APPLICANT: Face, Maurice
APPLICANT: Tracy, Maurice
APPLICANT: Spaulding, Vikk
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                               ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,632
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.3%; Score 40.2; DB 1; 1
60.6%; Pred. No. 0.21;
Live 0; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Genetics Institute, Inc.
87 CambridgePark Drive
                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05 07/956,937
FILING DATE: 05-0CT-1992
ATTORNEY/AGENT INFORMATION:
NAME: MILLS, DEMETRA J
RECISTRATION NUMBER: 34,506
REFERENCE/DOCKET NUMBER: 44.4-025B
TELECHONNIA.CATION INFORMATION:
TELECHONNIA.CATION INFORMATION:
TELECHONNIA. 703-684-1111
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 703-684-1124
INFORMATION FOR SEC ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH : 1897 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 60.6
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 11near
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cambridge
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HYPOTHETICAL: N
HATI-SENSE: NO
US-08-184-632-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-691-641-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            529 ctacatttgtggttattctcaccaaaatagtcagtgtaaggctgttactgtcctgttctt 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               589 gggaattttgattacattgatgactttcagcattattgaattattcatttctctgccttt 648
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Sequence 1. Application US/08184632

Patent No. 5646009

GENERAL INFORMATION:
PAPLICANT: RHOADS, ROBERT E
APPLICANT: RHOADS, ROBERT E
TITLE OF INVENTION: HYBRID VECTOR AND METHOD RESULTING IN
TITLE OF INVENTION: PROTEIN OVERPRODUCTION BY EUKARYOTIC CELLS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS: 1
ADDRESSEE: Lowe, Price, LeBlanc & Becker
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 3889;
                                                                                                                                                                                                                UPERATING SISTEM: DOS SOFTWARE: PACENTIN RELEASE #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: PAPPLICATION NUMBER: US/08/648,298
FILING DATE: 15-JUN-1996
CLASSIFICATION: 435
ATTORNEY-AGENT INFORMATION: NAME: Green, Reza REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4035/08865
TELECOMMUNICATION INFORMATION: TELEPHONE: 212527700
TELEFAX: 21253770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
5.3%; Score 40.4; DB 2; Length 3:
Best Local Similarity 48.7%; Pred. No. 0.23;
Matches 110; Conservative 0; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
TISSUE TYPE: Submaxillary gland
                                                                                                              ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3889 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                   ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: CDNA to MRNA
HYPOTHETICAL: NO
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
ORGANISM: HOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-184-632-1
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2178 GGTTCACATATCTGGATCTGTGTATTTGTACTTTAAATGTGACAAATAAACCTT 2237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     647 ttctcaattttggggtgccactcagaggattgtgattgtgaacaatgttgttgactagca 706
                                                                                                                                                                                                                                                                                                                                                     587 ttgggaattttgattacattgatgactttcagcattattgaattattcatttctctgcct 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08530165
Patent No. 5907081
GENERAL INFORMATION
APPLICANT: Isaac, Peter G.
APPLICANT: Roberts, Jeremy A.
APPLICANT: Coupe, Simon A.
TITLE OF INVENTION: Control of Plant Abscission and Pod Dehiscence
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39.2; DB 2; Length 2447;
Pred. No. 0.4;
1; Mismatches 84; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DEADED WISK
COMPUTER: DEADED WISK
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,165
FILING DATE: 32-SEP-1995
CLASSIPICATION B00
PROOR APPLICATION BATA:
APPLICATION NUMBER: PCT/GB94/00689
FILING DATE: 31-MAR-1994
FILING DATE: 31-MAR-1994
FILING DATE: 31-MAR-1993
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                  Query Match 5.2%;
Best Local Similarity 51.1%;
Matches 89; Conservative 1
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-014-969-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION:
US-08-530-165-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-08-530-165-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Racie, Lisa A.
APPLICANT: Racie, Lisa A.
APPLICANT: Recep, David
APPLICANT: Spaulding, Vikxi
APPLICANT: Spaulding, Vikxi
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: BROODING THEM
NUMBER OF SEQUENCES: 32
CORRESPONDENCE: 32
CORRESPONDENCE: Genetics Institute, Inc.
STREET: 87 Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.2%; Score 39.8; DB 1; Length 247;
65.9%; Pred. No. 0.13;
11ve 0; Mismatches 29; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691,641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,969
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Patent No. 5965397
GERERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BICOM, SCOLT.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 89824
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 BASE pairs
TENGTH: 247 BASE pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Sprunger, Suzanne A. REGISTRATION NUMBER: 41,323 TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : (617) 498-8284
(617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 65.99
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-691-641-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT, 14
US-09-014-969-14
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Search completed: August 30, 2002, 02:42:19 Job time: 7102 sec

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                                                                           ; Search time 214.01 Seconds
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                    hits satisfying chosen parameters:
                                                                                                                                                                                                                        1736436 seqs, 858457221 residues
                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                    OM nucleic - nucleic search, using sw model
                                                                           August 30, 2002, 01:33:42
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                       N_Geneseq_032802:*
                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                US-09-821-821-1
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114:
117:
118:
220:
21:
                                                                                                                                                                                                                                                     Total number of
                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                           Searched:
                                                                                                                                                             Sequence:
                                                                                Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	<u>+</u>		ap :				
Nesur.	No.	Score	Match	Match Length DB	DB	£	Description
;	-	760	!	760	22	!	Human CD20/IgE-rec
	7	730.2	96.1	747	22	AAH64741	Human secreted pro
υ	e	689.8			22	AAL01084	Human reproductive
	4	668.4			22	AAD18275	Human immune syste
	Ŋ	666.4			22	AAS04283	DNA sequence encod
	9	635.8			22	ABA09478	Human secreted pro
	7	598.2			22	AAS04279	Novel human membra
	8	351.2			21	AAC03080	Human secreted pro
	6	347.4			22	AAS04282	Novel human membra

30-MAR-2000; 2000US-193728P.

Novel human membra Novel human membra Human secreted pro Human secreted pro High affinity immu Human high affinit Human full-length		HTm4 protein codin HTm4 gene. Homo s Clone CD20.4 encod CD20.4 eDNA. AAN Human CD20.4 antig Human CD20.4 antig Human CD20.4 antig	Umphocyte CDNA. AAN9 CD20 antige CD20 antige CD20 antige CD20 antige CD20 antige	Human lymphocyte c Extended human sec Dendritic cell (DC Human secreted pro Human secreted pro Dendritic cell (DC Human secreted pro Human secreted pro Human protein enco
22 AAS04281 22 AAS04280 22 AAN6445 21 AAA16693 21 AAX15104 21 AAX35842 22 AAK94442	22 AAK92131 22 AAK93395 22 ABA09445 23 AAS83423 21 AAZ36238 22 AAF77694	17 AAT45120 19 AAV03875 13 AAQ21170 10 AAW90610 17 AAT14710 20 AAV81206 21 AAA50584	10007001	2.0 AAX97730 2.2 AAX97730 2.2 AAD19723 2.1 AAX52580 2.2 AAD19722 2.2 ABA09233 2.2 AAH99750
417 246 468 1330 1669 1670	822 822 562 1710 1563	1661 1661 1474 1474 1474 1474	1474 1476 1476 1476 1476 1476	1476 1060 932 945 1001 1036 1106
44.8 31.9 30.7 11.4 11.4	10.4 10.4 9.1 8.5 8.2	88.1 7.7.7 7.7.7 7.7.7		7.7.7.7.7.7.7.1.1.1.1.1.1.1.1.1.1.1.1.1
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10 11 12 13 14 15	17 18 19 20 21 22	23 25 25 26 26 27 27	26 57 4 33 2 1 1 C	8 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

ALIGNMENTS

AAD21441 standard; cDNA; 760 BP

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RESULT

AAD21441

AAD21441;

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Human; CD20/IgE-receptor like protein; immunoglobulin E; agp-96614-al; agp-69406-al; cancer; abnormal cell proliferation; autoimmune disease; ovarian cancer; brain cancer; arteriosclerosis; vascular restenosis; rheumatoid arthritis; multiple sclerosis; allergy; dernatitis; asthma: reproductive disease; diabetes; transplant rejection; endometriosis; infertility; gene therapy; ss.
                                                  Human CD20/IgE-receptor like protein encoding cDNA, agp-96614-al.
                                                                                                                                                                                                                            /*tag= a
/product= "Human CD20/IgE-receptor like protein,
agp-96614-al"
                                                                                                                                                                                          Location/Qualifiers
98..700
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                         28-JAN-2002 (first entry)
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                                                                                                                                                                         Homo sapiens
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XX (AMCE-) AMGEN INC.
XX

Welcher AA, Calzone FJ;
XX

Welcher AA, Calzone FJ;
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WPI; 2001-662968/76.

PT defeating or preventing diseases associated with the polypeptide useful for treating antaquoists and antibodies of the polypeptide useful for treating pr amtagonists and antibodies of the polypeptide useful for treating pr amtagonists and antibodies of the polypeptide useful for treating pr amtagonists and antibodies of the polypeptide useful for treating e.g. cancer, asthma .

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CLaim 1; Fig 1; 145pp; English.
XX

CC the invention relates to human CD20/immunoglobulin E (IGE)-receptor cC ulcle polypeptides designated as agp-96614-al and agp-6446-al and nuclei acid molecules encoding such polypeptides. Polypeptides of the invention are useful for treating, preventing or ameliorating attentiosclerosis, vascular restenosis; pathology from allergens cC arteriosclerosis, vascular restenosis; pathology from allergens such as sheumatoid arthritis, autoimmune disease, multiple sclerosis, diabetes, transplant rejection and reproductive diseases such as conferentially, preterm labour and delivery, endometriosis etc. They are also useful for identifying antegonists and as immunogens, for raising antibodies which may also be used to prevent, treat or raising antibodies which may also be used to prevent, treat or raising antibodies which may also be used to prevent, treat or raising antibodies which may also be used to prevent, treat or raising antibodies which may also be used to prevent, treat or raising antibodies which may also be used to prevent, treat or raising antibodies which may also be used to prevent, treat or raising antibodies which may also be used to prevent, treat or raising antibodies of the provent of diseases and as phybridistation probes.

CC They are also useful in gene therapy. The present sequence is human CD20/IgE-receptor like protein encoding CDN, age-respector is human CD20/IgE-receptor like protein encoding CDN, age-respector like protein encoding CDN, age-respector like protein encoding
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                                    ctaaatcatctcctttcaaattatcaccgaccatcatggattcaagcaccgcacacag
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                                                                                                                  ttcagccacgaccttttcaactcaaagcccttgcaaaaattatttgctagaaaatgaa
                                                                                                                        attotggggctctgtttgttcattaattctggagccttcctaattgcagtgaaaagaaa
 Length 760;
                Indels
100.0%; Score 760; DB 22;
100.0%; Pred. No. 5.2e-165;
ive 0; Mismatches 0;
       Best Local Similarity 100.0%;
Matches 760; Conservative
Query Match
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potentially secreted proteins. The nucleic acids and the polypeptides diseases associated with inappropriate GRNSET gene expression. For example, they be used in the prevention, treatment and diagnosis of GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or deletions in a patient's genome that affect the activity of GENSET or by supplementing the patients own production of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate GENSET expression by binding with the cells' own genes and preventing their expression. The sense and antisense nucleic acids may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to determine which patients may be in need of restorative therapy.
                                                                                                                      099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety oi diseases, and for diagnosis of those diseases.
              gtgccactcagaggattgtgattgtgaacaatgttgttgactagcactgtgagaataaag
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                                                                                                                                   ttattctcaccaaaatagtcagtgtaaggctgttactgtcctgttcttgggaattttgat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Page 576-577; 921pp; English.
                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                           AAH64741 standard; cDNA; 747
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein cDNA,
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Human; reproductive system related antigen; reproductive system disorder;
Human reproductive system related antigen cDNA SEQ ID NO: 1085
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2000US-0229345.
2000US-0229513.
2000US-0230437.
2000US-0231438.
2000US-0231243.
2000US-0231243.
2000US-0231244.
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20000S-0232081.
20000S-0231968.
20000S-0232397.
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2000US-0233064.
2000US-0233065.
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2000US-0225270.
2000US-022547.
2000US-0225757.
2000US-0225757.
2000US-0225759.
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2000US-0227009.
2000US-0228924.
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2000US-0184664.
2000US-0184564.
2000US-0186350.
2000US-0198174.
2000US-0198123.
2000US-0198123.
2000US-020515.
2000US-020515.
2000US-0214886.
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2000US-0224519.
2000US-0225213.
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2000US-0226868.
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2000US-0229343.
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                        cancer; gene therapy; ss
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08-SEP-2000;
08-SEP-2000;
12-SEP-2000;
14-SEP-2000;
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08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
                                                     WO200155320-A2
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26 - 70L - 2000;
14 - 70L - 2000;
14 - AUG - 2000;
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01-SEP-2000;
01-SEP-2000;
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22-MAR-2000;

17-MAR-2000;

18-APR-2000;

18-APR-2000;

19-MAY-2000;

20-JUN-2000;

20-JUN-2000;

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20-JUN-2000;

21-JUL-2000;

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                                        Homo sapiens
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                                                                                                                                                                                    The GENSET polypeptides may be used as antigens in the production antibodies and in assays to identify modulators (agonists and antagonists) of GENSET polypeptide expression and activity. The present sequence is a GENSET nucleic acid of the invention.
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0
                                                            Score 730.2; DB 22; Length 747; Pred. No. 3.5e-158; 0; Mismatches 3; Indels 0;
                                       Sequence 747 BP; 240 A; 145 C; 121 G; 241 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
AAL01084/c
ID AAL01084 standard; CDNA; 737
                                                              / Match 96.1%;
Local Similarity 99.6%;
nes 732; Conservative (
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21-SEP-2000; 2000US-0234234.

25-SEP-2000; 2000US-0234937.

25-SEP-2000; 2000US-0234937.

26-SEP-2000; 2000US-0235484.

27-SEP-2000; 2000US-0235834.

29-SEP-2000; 2000US-0235834.

29-SEP-2000; 2000US-0235836.

29-SEP-2000; 2000US-0235836.

29-SEP-2000; 2000US-0235836.

29-SEP-2000; 2000US-0235836.

29-SEP-2000; 2000US-0235836.

29-SEP-2000; 2000US-0235836.

29-SEP-2000; 2000US-023636.

29-SEP-2000; 2000US-023636.

29-SEP-2000; 2000US-023636.

29-SEP-2000; 2000US-023636.

20-CCT-2000; 2000US-023636.

20-CCT-2000; 2000US-023636.

20-CCT-2000; 2000US-023636.

20-CCT-2000; 2000US-023636.

20-CCT-2000; 2000US-023636.

20-CCT-2000; 2000US-02366.

20-CCT-2000; 2000US-0246.

20-CCT-2000; 2000US-0249.

20-CCT-20
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Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
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                                                                                                                                                                                                                                                                                 737 GACTGAAGTACCAACTAAGTCATCTCCTTTCAAATTATCACCGACACCATCATGGATTCA 678
                                                                                                                                                                                                                                               Gaps
                                                                                                                                            The present invention provides the protein and coding sequences of number of human reproductive system related antigens. These can be in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a coding sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gagtecacagaactttcagecacgacettttcaactcaaageceettgcaaaattattt
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                                                                                                                                                                                                                            Length 737;
                                                                                                                            Claim 1; SEQ ID NO 1085; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                 Sequence 737 BP; 240 A; 128 C; 152 G; 217 T; 0 other;
                                                                                                                                                                                                                           90.8%; Score 689.8; DB 22; 98.9%; Pred. No. 6.4e-149; iive 0; Mismatches 7; i
                                                     Ruben SM;
                                    (HUMA-) HUMAN GENOME SCI INC
08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
                                                                                                                                                                                                                                   Best Local Similarity 98.9
Matches 705; Conservative
                                                     Barash SC,
                                                                      WPI; 2001-465570/50.
P-PSDB; AAM95114.
                                                     Rosen CA,
                                                                                                                                                                                  invention
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                                                                                                                                                                                                                                   cancer; Gaucher's disease; viral hepatitis; gene therapy; cytostatic; diabetes mellitus; arrhythmia; wound healing; ischaemic lesion; AIDS; Acquired Immune Deficiency Syndrome; virucide; hepatotropic; vasotropic; autoimmune disorder; inflammation; cardiovascular disorder; hair loss; wound healing; cell proliferation; skin aging; endocrine disorder;
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                                                                                                                                                                                         Human immune system-related protein-encoding gene 9 cDNA clone HTENN45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ebner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated immune system-related polypeptide useful for treating rheumatoid arthritis, AIDS, allergy, cancer, Gaucher's disease, diabetes mellitus, arrhythmia, wound healing, ischemic lesions and viral hepetitis.
                                                                                                                                                                                                                      system-related protein; allergy; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                               /product= "Human immune-system related protein"
   759
DR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moore PA,
                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
29..634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JJ, Moore
Ruben SM;
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                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC.
                                                                                                     AAD18275 standard; cDNA; 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-187873P.
2000US-224367P.
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                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kenny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ni J, Hilbert D, Kenny
Gruber JR, Endress GA,
                                                                                                                                                                                                                                                                                                            food preservative; ss
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P-PSDB; AAE10917.
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                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                    AAD18275;
   707
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                                                                                       AAD18275
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biolog. The present sequence represents a human immune-system related protein-encoding cDNA of the invention.
                                                                                        Gaps
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                                                                                                               70 ctcctttcaaattatcaccgacaccatcatggattcaagcaccgcacacagtccggtgtt
                                                                                                                          aactctgataatattgagccgaataatgaattttcttagtgccctgggagcaatagctgg
                                                                                                                                                                                                    gaccttttcaactcaaagccccttgcaaaattatttgctagaaaatgaaaatcttagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              membrane receptor; IgE receptor; CD20;
                                                                                        Ä
                                                                  689;
                                                                   Length
                                                                                        Indels
                                T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence encoding novel human membrane protein.
                                                                  22;
                                                                                          9:
                                                                   Score 668.4; DB 2;
Pred. No. 5.1e-144
                                                                                          0; Mismatches
                                 BP; 204 A; 138 C; 114 G; 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP
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                                                                   87.9%;
99.0%;
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physiological disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                          Matches 683; Conservative
                                                                              Similarity
                                   Sequence 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-SEP-2001
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WO200157188-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                             ABA09478;
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                                                                                                                                                                                                           The present sequence encoding for a novel human membrane protein includes the flanking 5'- and 3'- sequences. Four amino acid sequences for novel human membrane proteins (AMO1210-AMO1213) are given in the present invention. These membrane proteins abare structural similarity with membrane receptors such as the IgE receptor and mammalian CD20. The novel human membrane proteins are useful for identifying agonist, antagonist and modulators of the membrane proteins, and for producing antibodies specific to the membrane proteins. The membrane proteins can be used for diagnosia, drug screening, pharmacogenomic applications, and diseases. The polynucleosides encoding the membrane proteins can be used to generate PCR primers or probes to identify mutations associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                       305
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                                                                                                                                           Polynucleotide encoding novel human membrane protein, useful for identifying agonist, antagonist or modifiers or for producing antibodies useful in therapeutic, diagnostic and pharmacogenomic
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                                                                                                                                                                                                                                                                                                                                                                             87.7%; Score 666.4; DB 22
99.1%; Pred. No. 1.5e-143;
ive 0; Mismatches 6;
                                                                                                                                                                                           Disclosure; Page 31-32; 32pp; English
                                                                                     (LEXI-) LEXICON GENETICS INC
                                                                 99US-0171567.
                                             12-DEC-2000; 2000WO-US33742
                                                                                                                                                                                                                                                                                                                               a particular disease.
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                       Turner CA;
                                                                                                                         WPI; 2001-408646/43.
                                                                                                                                                                                                                                                                                                                                                                                      Similarity
         WO200146417-A2.
                                                                22-DEC-1999;
                                                                                                                                                                         applications
                           28-JUN-2001.
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                                                                                                      Walke DW,
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Best Local S
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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss.
ctggaatcattctcctcacatttggtttcatcctagatcaaaactacatttgtggttatt 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cytokine; cell proliferation; cell differentiation; growth fanactopiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolyysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopath; chronic inflammatory heart disease; arterial ischemia; bone disorder; osteoporosis; vascular growth disorder; cissue regeneration; wound healing; infection; immune disorder; antissue aregeneration; wound healing; antisniamatory; antisathmatic; antisticherissclerotic; antistinflammatory; antistinflammatory; antistinflammatory; antistinflammatory; antistinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oteins and DNA encoding sequences useful for preventing, or ameliorating a medical condition in a mammalian subject
                                                                      ctcaccaaaatagtcagtgtaaggctgttactgtcctgttcttgggaattttgattacat
                                                                                                              tgatgactttcagcattattgaattattcatttctctgcctttctcaattttggggtgcc
                                                                                                                                                                                                                                                                                                                                                                                  actcagaggattgtgattgtgaacaatgttgttgactagcactgtgagaataaagatgtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted protein homologue-encoding cDNA, SEQ ID NO:1254.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABA09478 standard; cDNA; 695 BP.
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27-APR-2000; 2000US-0560875.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; ABB12234.
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703 agcactgtgagaataaagatgtgttaaaatctcaa 737

ccttt-ctcaattttggggtgccactcagaggattgtgattgtgaacaatgttgttgact

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collypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutica applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities, including cytokine, cell proliferation or cell differentiation activity; activin- or inhibin-related activities; had man activity; insue growth activity; insue growth activity; insue growth activities; comparation or chemotric or chemokinetic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis.

CC thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis.

CC beending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders, bone disorders (e.g., myeloid or lymphoid cell cancers, haematopoietic disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and vascular growth. Polypeptides may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with chaling (e.g., of burns, incisions and ulcers), while those with growth factor activity may be used to promote cell growth. For example, such polypeptides may be used to commote burned to promote cell growth. For example, such polypeptides may be used to commote the planter of require to growth properties of require to neuroepithalial cells and the planter of required to mental cancer of any properties of required to receive the mells of required to receive the cells and the planter of required to remore planterial and control or repetited to remore planterial and properties and or required to remore planterial cance autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug The present sequence represents a cDNA encoding a polypeptides of the invention. Although novel, many of the can be used to augment or replace cells damaged by illness, novel human polypeptide of the invention. techniques. screening that

Sequence 695 BP; 203 A; 142 C; 116 G; 234 T; 0 other;

4 421 agtgccctgggagcaatagctggaatcattctcctcacatttgagtttcatcctagatca 480 aaactacatttgtggttattctcaccaaaatagtcagtgtaaggctgttactgtcctgtt 585 agcaccgcacacagtccggtgtttctggtatttcctccagaaatcactgcttcagaatat 166 tttggagttatcttccttttcactttgttaaaaccatatccaaggtttccctttatattt 346 gactgaagtaccaactaaatcatctcctttcaaattatcaccgacaccatcatggattca 106 61 agcaccgcacacagtccggtgtttctggtatttcctccagaaatcactgcttcagaatat 120 gagtecacagaaettteagecacgaeetttteaaeteaaageeeettgeaaaattattt 226 gctagaaaaatgaaaatcttagggactatccagatcctgtttggaattatgaccttttct 286 gctagaaaaatgaaaatcttagggactatccagatcctgtttggaattatgaccttttct 240 ctttcaggatatccattctggggctctgttttgttcattaattctggagccttcctaatt 406 Gaps 1 gactgaagtaccaactaagtcatctcctttcaaattatcaccgacaccatcatggattca 60 agtgccctgggagcaatagctggaatcattctcctcacatttg-gtttcatcctagatca 4; y Match 83.7%; Score 635.8; DB 22; Length 695; Local Similarity 98.4%; Pred. No. 1.5e-136; hes 684; Conservative 0; Mismatches 7; Indels 4; Query Match Best Local Si Matches 684; 121 287 347 526 47 107 167 227 181 qq 셤 g δ g ŏ 셤 ð g ò đ δ ò 셤 δ á

Sequence 603 BP; 162 A; 125 C; 104 G; 212 T; 0 other;

The present sequence encodes for novel human membrane protein #1. Human membrane proteins #1 so f 4 human membrane proteins (AADU1210-AADU1213) given in the present invention. These membrane proteins share structural similarity with membrane receptors such as the IgE receptor and mammalian CD20. The novel human membrane proteins are useful for identifying agonists, antagonists and modulators of the membrane proteins, and for producing antibodies specific to the membrane proteins. The membrane proteins can be used for diagnosis, and the treatment of physiological disorders and diseases. The polynucleotides encoding the membrane proteins can be used to generate polynucleotides encoding the membrane proteins can be used to generate profession or probes to identify mutations associated with a particular Polynucleotide encoding novel human membrane protein, useful for identifying agonist, antagonist or modifiers or for producing antibodies useful in therapeutic, diagnostic and pharmacogenomic Human; membrane protein; membrane receptor; IgE receptor; CD20; physiological disorder; ss. /*tag= a
/product= "Human membrane protein #1"
/transl_except= (pos:595..600,aa:Cys) Novel human membrane protein #1 cDNA sequence. Location/Qualifiers Claim 1; Page 29; 32pp; English. BP. AAS04279 standard; cDNA; 603 (LEXI-) LEXICON GENETICS INC. 99US-0171567. 12-DEC-2000; 2000WO-US33742. (first entry) 1..603 /*tag= Walke DW, Turner CA; WPI; 2001-408646/43. P-PSDB; AAU01210 WO200146417-A2 Homo sapiens 22-DEC-1999; applications 28-JUN-2001. 26-SEP-2001 AAS04279; disease AAS04279 a

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nucleic acid that is a 5' expressed sequence tag (5' EST) faining CDNAs and genomic DNAs that correspond to 5'ESTs and
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ID AASO4282 standard;
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         DB 22;
         Score 598.2; DB 22
Pred. No. 6.2e-128;
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                     0; Mismatches
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99.58;
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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain processin regulatory sequences and to design expression and secretion
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96.8%; Pred. No. 2.4e-71;
11ve 6; Mismatches 5;
                                                                                                       Claim 1; SEQ ID 3078; 71pp + CD-ROM; English.
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                        Human; membrane protein; membrane receptor; IgE receptor; CD20; physiological disorder; ss.
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                                                                                                                                                      /product= "Human membrane protein #4"
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Novel human membrane protein #4 cDNA sequence
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                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                            (LEXI-) LEXICON GENETICS INC.
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Matches 354; Conservative
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Polynucleotide encoding novel human membrane protein, useful for identifying agonist, antagonist or modifiers or for producing antibodies useful in therapeutic, diagnostic and pharmacogenomic
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llarity 99.1%; Pred. No. 8.3e-69;
Conservative 0; Mismatches 3; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                           AAS04281 standard; cDNA; 417 BP
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/*tag= a
/product= "Human
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physiological disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                 Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety of diseases, and for diagnosis of those diseases
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                                                                                                                                                                                                                              Score 242.8; DB 22;
Pred. No. 1.6e-46;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Page 581; 921pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                              31.9%;
99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH64745 standard; cDNA; 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-DEC-1999; 99US-0169629.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-DEC-2000; 2000WO-IB01938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                               Local Similarity 99.2 es 244; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-367870/38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tgttga 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tgttga 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; secr
GENSET; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH64745;
                                                                                                                                                                                                                                Query Match
                                                                                                                                   disease
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Matches
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Homo sapiens.

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The invention relates to full length GENSET human nucleic acids encoding potentially secreted proteins. The nucleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or deletions in a patient's genome that affect the activity of GENSET or by supplementing the patients own production of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate atteins rexpression. The sense and antisense nucleic acids may also be their expression. The sense and antisense nucleic acids may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to determine which patients may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antibodies and in assays to identify modulators (agonists and antibodies and sequence is a GENSET polypeptide expression and activity. The present sequence is a GENSET nucleic acid of the invention.
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Sequence 468 BP; 155 A; 94 C; 81 G; 138 T; 0 other;

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                                                                                                                                                                                  203 caaagcccttgcaaaaattatttgctagaaaaatgaaaatcttagggactatccagatc 262
                                                                                                                                                                                                                                                                         181 caaagccccttgcaaaaattatttgctagaaaatgaaaatcttaggggatatccattct 240
                                                                                                                                                                                                                                                                                                       ctgtttggaattatgaccttttctttttggagttatcttccttttcactttgttaaaacca 322
                                                                                                                                       241 ggggctctgttttgttcattaattctggagccttcctaattgcagtgaaaagaaaaacca 300
                                                                                                                         83 atcaccgacaccatcatggattcaagcaccgcacagtccggtgtttctggtatttcct 142
                               Gaps
                                                            23 agcacaagaaaagaacatggtctagactgaagtaccaactaaatcatctcctttcaaatt 82
                                                                             ő
30.7%; Score 233.4; DB 22; Length 468; 80.5%; Pred. No. 2.6e-44; ive 0; Mismatches 66; Indels 0;
              ,'6e-44;
es 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 301 cagaaactctgggaattttgattacattgatgactttca 339
                                                                                                                                                                                                                                                                                                                                                                     323 tatccaaggtttccctttatattttctttcaggatatcca 361
                                  Matches 273; Conservative
                    Similarity
    Query Match
                      Local
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AAA16693 standard; cDNA; 1330 BP
                     16-JUN-2000 (first entry)
             AAA16693;
   AAA16693
RESULT
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Human secreted protein clone pe246_1 nucleotide sequence SEQ ID NO:151

Human; secreted protein; immunestimulant; immunesuppressant; virucide; antibacterial; antifungal; cytostatic; antiinflammatory; dermatological; antidabetic; antiasthmatic; antiarhribeumatic; protozoacide; antithyroid; immune deficiency; severe combined immunedeficiency; SCID; infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus; connective tissue disease; multiple sclerosis; erythematosis; chiematical arthritis; autoimmune pulmonary inflammation; asthma; duillain-Barre syndrome; autoimmune pulmonary inflammation; asthma; insulin dependent diabetes mellitus; graft-versus-host-disease; autoimmune inflammatory eye disease; allergy; ss.

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Gaps

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aaaaattatttgotagaaaaatgaaaatottagggactatccagatcctgtttggaatta 275

Conservative

Matches 232;

216

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485 agaagttettgaagggagaacecaaagteettgggggttgtgeagattetgaetgeeetga

tgaccttttctttttggagttatcttccttttcactttgttaaaaccatatccaaggtttc 335

545

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276

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AAA16618 to AAA16697 encode the human secreted proteins given in AAY94898 to AAY94980, isolated from human adult brain, adult thyroid, adult retina, foetal carcinoma, adult blood, adult neural, foetal kidney, adult placenta, adult testis, whole embryo, adult uterus, adult tumour, foetal brain, adult thymus, foetal placenta, adult uterus, adult tumour, and adult bladder, cDNA libraries. The polynuclectides and proteins are predicted to have blological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. The polynuclectides can be used as markers for tissues in which the protein is preferentially expressed, as molecular weight arreadment of immune deficiencies and disorders, such as severe combined transment of immune deficiencies and disorders, such as severe combined immunedeficiency (SCID), as well as viral, bacterial, fungal and other infections. These infections include human immunodeficiency virus (HIV), hepatitis, herpesviruses, mycobacteria, Leismania spp, malaria and carchinaria. The proteins can be used to treat autoimmune disorders such as connective tissue disease, multiple sclerosis, systemic lupus crythematosis, rheumatoid arthritis, autoimmune pulmonary inflammatin corrections inclimmune pulmonary inflammatory ed disease. The proteins can also be used to treat allergic conditions, such asthma. AAA1674 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides encoding secreted proteins, which may have e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probes for the human secreted proteins from the present invention.
                                                                                                                                                                                                                                                                                                                                                                       Spaulding V;
                                                                                                                                                                                                                                                                                                                                                        Evans C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nutritional, chemokine, immune stimulating or suppressing, hematopoiesis regulating, tissue growth, activin/inhibin antiinflammatory or tumor inhibition activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.4%; Score 86.4; DB 21; Length 51.1%; Pred. No. 1.7e-10; Live 0; Mismatches 216; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1330 BP; 364 A; 285 C; 309 G; 372 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                        Collins-Racie LA,
Steininger RJ, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 160; Page 606-607; 641pp; English.
                                                                                                                                                                                                                                                                                                                                                      LaVallie ER,
, Agostino MJ,
Fechtel K;
                                                                                                                                       98US-0096622.
                                                                                                                                                                           98US-0099229.
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                                                                                                                                                                                                                                                                99US-0132020
                                                                                                                                                                                                                                                                                 99US-0096622
                                                                                                      99WO-US18298
                                                                                                                                                                                                                                                                                                                      (GEMY ) GENETICS INST INC.
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Clark HF, F
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                         McCoy JM,
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-205979/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAY94973
                                   WO200009552-A1.
                                                                                                                                                                                                            08-JAN-1999;
12-FEB-1999;
18-FEB-1999;
30-APR-1999;
                                                                                                      13-AUG-1999;
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                                                                                                                                                                                                                                                                                     11-AUG-1999
                                                                                                                                                                            04-SEP-1998
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us-09-821-821-1.rng

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High affinity immunoglobulin E receptor-like protein; IGERB; Incyte clone 927955; inflammatory response; AIDS; Addisons's disease; atherosclerosis; bronchitis; ulcerative colitis; diabetes mellitus; emphysema; gout; Graves's disease; osteoporosis; rheumatoid arthritis; Sjogren's syndrome; cancer; ss.
                                                                                                                                                                                                                            570 otgitacigicoigitotigggaaittigatiacaitgaigaciticagcaitaitgaai 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotide coding for high affinity immunoglobulin E receptor-like protein - and its complement, useful for diagnosis, prevention and antisense therapy of inflammatory responses
                  tgaatatcaccagctctgtactggctgcatcagggatcttaatcaaccacatttagcttgg
                                                                                                                                                                                                  cgttttattcattccatcaccttactgtaactactatggcaactcaaataattgtcatg
                                                                                                                                                                                                                                                        ggactatgtccatcttaatgggtctggatggcatggtgctcctcttaagtgtgctggaat
 cctttatattttctttcaggatatccattctgggggctctgttttgttcattaattctggag
                                                                                                                tgaattttcttagtgccctgggagcaatagctggaatcattctcctcacatttggtttca
                                                                                                                                                                       tcctagat----caaaactacatttgtggttattctcaccaaaatagtcagtgtaagg
                                                         cottoctaattgcagtgaaaagaaaaccacagaaactotgataatattgagccgaataa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High affinity immunoglobulin E receptor-like protein (IGERB) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes a high affinity immunoglobulin E receptor-like protein (IGERB). The present sequence was first identified in Incyte clone 927955 for the brain cDNA library
                                                                                                                                                                                                                                                                                                                totgcattgctgtgtccctctctgcctttggatg 938
                                                                                                                                                                                                                                                                                     tattcatttctctgcctttctcaattttggggtg
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159..878
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/product= IGERB
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                                                                                                                                                                                                                                                                                                                                                                                   AAX15104 standard; cDNA; 1669
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336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  515
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                                                                                                                                                                                                                                                                                                                                     216 aaaaattatttgctagaaaaatgaaaatcttagggactatccagatcctgtttggaatta 275
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BRAINOTO4. Polynucleotides complementary to the IGERB CDNA can be used as probes to IGERB gene expression. IGERB proteins and nucleotides may be used for the diagnosis of inflammatory responses associated with expression of IGERB, e.g. AIDS. Addisons's disease, atherosclerosis, bronchitis, ulcerative colitis, diabetes mallitus, emphysema, yout, Garves's disease, osteoporosis, rheumatoid arthritis, Sjoyren's syndrome and complications of cancer. The sequences may also be useful in assays that detect activation or
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                            | || || || || || 325 agaagttcttggaggtggagattcttggactgcctga
                                                                                                                                                                                                                                                                                                                                                                                                              tgaccttttcttttggagttatcttccttttcactttgttaaaaccatatccaaggtttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                     385 tgagccttagcatgggaataacaatgatgtgtatggcatctaatacttatggaagtaacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              565 tgaatatcaccagctctgtactggctgcatcagggatcttaatcaacacatttagcttgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cgttttattcattccatcaccttactgtaactactatggcaactcaaataattgtcatg
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                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                      Length 1669;
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                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                Sequence 1669 BP; 481 A; 350 C; 334 G; 501 T; 3 other;
                                                                                                                                                                                                                                                      Score 86.4; DB 20;
Pred. No. 1.8e-10;
); Mismatches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  630 tattcatttctctgcctttctcaattttggggtg
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160..879
/*tag= a
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                                                                                                                                                           induction of various cancers.
                                                                                                                                                                                                                                                      11.48;
51.18;
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                                                                                                                                                                                                                                                                                                232; Conservative
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                                                                                                                                                                                                                                                           Query Match
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/product= "Human IGERB"
                    98US-0213389
                           97US-0916902
                                 (INCY-) INCYTE PHARM INC
                                        Bandman O, Corley NC,
                                              WPI: 2000-012123/01
                                                  P-PSDB; AAY50174
                           21-AUG-1997;
                    15-DEC-1998;
       US5977072-A
              02-NOV-1999
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rinis sequence represents curva encouling integral minimum integration of (IGER). Consents. An allergic response is initiated by release of IGERB were initially identified in a brain consents, this sequence being a consensus. An allergic response is initiated by release of IGERB were from B lymphocytes. The IGE molecules then bind to the high affinity igE receptor (FoRI) present on mast cells and basophils, which triggers the release of histamine and proteases from cytoplasmic granules and least to the synthesis of effectors of the allergic and inflammatory response, such as prostaglandins, leukotrienes and cytokines. As IGERB binds IGE, it may be administered to stimulate allergic and immune cresponses in patients in whom IGERB is under expressed or inactive and to supplement the patients own production of the protein. IGERB may also be used as an antigen for the production of antibodies and activity. The antibodies may also be used in diagnosis. Antibodies and antagonists of may be administered to downregulate IGERB activity and reduce the potency of inflammatory disorders such as multiple sclerosis, candington as the antibodies and allergic responses. They may be used in this way to treat inflammatory disorders such as multiple sclerosis, categorists may be used to enhance immune responses. This sequence represents cDNA encoding human high affinity immunoglobulin High affinity immunoglobulin E receptor-like protein useful for stimulating allergic and immune responses -Sequence 1670 BP; 481 A; 350 C; 334 G; 501 T; 4 other; Example 5; Fig 1; 29pp; English.

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                                                216 aaaaaattattigctagaaaaatgaaaatcttagggactatccagatcctgtttggaatta 275
                                                                   tgaccttttcttttggagttatcttccttttcactttgttaaaaccatatccaaggtttc 335
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11.4%; Score 86.4; DB 21; Length 1670;
51.1%; Pred. No. 1.8e-10;
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Search completed: August 30, 2002, 02:46:09 Job time: 4347 sec

<u>ь</u> Lal

Tue Sep 3 13:14:37 2002

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Sequence Sequence Homo sapi

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Run on:

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Database

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J05019 Mouse mast
L135848 Homo sapten
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AR082014 Sequence
BD003343 HT m4 , m
125809 Sequence 3
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107272 Sequence 19
X12530 Human mRNA
I07277 Sequence 24
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AC015840 Homo sapi
AP003127 Homo sapi
AP001034 Homo sapi
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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[ (sites)
Welcher, A.A. and Calzone, F.J.
Cd20/ige-receptor like molecules and uses thereof
Patent: WO 0174903-A 1 11-0CT-2001;
Amgen, Inc. (US)
Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
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                                                                                                                                            August 30, 2002, 00:42:07; Search time 1960.86 Seconds (without alignments) 8110.813 Million cell updates/sec
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/product="MS4A5 protein"
/product="MS4A5 protein"
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/db_xref="d1:1364940!
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VLFGGIITLMTFSIIEFTSLFFSILGGHSEDCDCEQCC"
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Catarrhini; Hominidae;
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expressed
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                                                                   Liang, Y. and Tedder, T.F.
Identification of a cd20-, fcepsilonribeta-,
family: sixteen new ms4a family members expre
                                                                                                                                                                                                                                                                                                                                                                             Score 689.2; DB 9;
Pred. No. 1.1e-145;
0; Mismatches 3;
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Durham, NC 27710, USA

    694 //Organism="Homo saplens"
/db_xref="taxon:9606"

                                                                                                               Genomics 72 (2), 119-127 (2001)
                                     Chordata;
Primates;
                                                                                                                                                                                     Location/Qualifiers
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Liang, Y. and Tedder, T.F.
                                                                                                                                                                                                                                                 /codon_start=1
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                         Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                          (bases 1 to 694)
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Submitted (24-FEB-
Dr., Durham, NC 27
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/protein_id="CAD10310.1"
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RKMKILGTIQLIEGIMFPESFOVIELFTLLKPVPPRFPIFLSGYPFWGSVLFINSGAFL
RKWKITETLIILSRIMNFLSALGAIAGIILLTPGFILDQNYICGYSHQNSQCKAVT
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Pred. No. 1.2e-161;
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3 (bases 1 to 691)
Ishibashi, K.
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/blostein_id="Aak01641.1"
/bloxref="d1:12696802"
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RKMKILGTIQILEGIMTFSFGVIFLFTLLKPYPRFPFIFLSGYPFWGSVLFINSGAFL
IAVKRTTETLITLAFINFLSALGAIAGIILLTFGFFLLDQNYICGYSHQNSQCKAVT
VILLGTILTLAFFSIIELFSLPFSILGGHSEDCDCEQCC"
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                                                                                                                                                                           AF321127 697 bp mRNA linear PRI 07-FEB-2001 Homo sapiens testis-expressed transmembrane-4 protein (TETM4) mRNA, complete cds.
                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 697)
Hulett,M.D., Pagler,E., Hornby,J.R., Hogarth,P.M., Eyre,H.J.,
Baker,E., Crawford,J., Sutherland,G.R., Ohms,S.J. and Parish,C.R.
Isolation, tissue distribution, and chromosomal localization of a novel testis-specific human four-transmembrane gene related to CD2 and FoepsilonRI-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (14-NOV-2000) Division of Immunology and Cell Biology,
John Curtin School of Medical Research, Mills Road, Canberra, ACT
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/product="testis-expressed transmembrane-4
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Pred. No. 2.9e-145;
0; Mismatches 6;
                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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57. .659
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Best Local Similarity 99.1%;
Matches 691; Conservative 0
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Hulett, M.D.
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Direct Submission
Submitted (20-APR-1998) Kenichi Ishibashi, Tokyo Medical and Dental
Submitted (20-APR-1998) Kenichi Ishibashi, Tokyo Medical and Dental
University, 2nd Internal Medicine; Yushima 1-5-45, Bunkyo, Tokyo
113-8519, Japan (E-mail:kishibashi.med2@med.tmd.ac.jp,
Tel:81-3-5803-5223, Fax:81-3-5803-0132)
Icoation/Qualifiers
1. 691
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Stablashl.K., Suzuki,M., Sasaki,S. and Imai,M.
Identification of a new multigene four-transmembrane family
related to CD20, HTm4 and beta subunit of the high-affinity
ttcttagtgccctgggagcaatagctggaatcattctcctcacatttggtttcatcctag
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Ishibashi,K., Sasaki,S. and Marumo,F.
Cloning of three CD20 homolog from human, ]
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Gene 264 (1), 87-93 (2001)
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Location/Qualifiers
                         GI:15132148
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99.18;
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                                         Homo sapiens
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Best Local Similarity
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                                                                                                        90.3%; Score 686.2; DB 9;
99.6%; Pred. No. 5.4e-145;
11ve 0; Mismatches 3;
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="testis"
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/gene="MS4A5"
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                                 /gene="MS4A5"
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Walke, D.W. and Turner, C.A.

Human membrane proteins and polynucleotides encoding the shaving homology to cd20 proteins and ige receptors Patent: WO 0146417A, 9 28-UNV-2001;

Lexicon Genetics Incorporated (US) cagaaactctgataatattgagccgaataatgaattttcttagtgccctgggagcaatag PAT ; 676; linear Length Indels Score 666.4; DB 6; Pred. No. 1.6e-140; DNA 0; Mismatches 231 /organism="Homo sapiens" /db_xref="taxon:9606" 140 c 112 g 231 AX179789 676 bp Sequence 9 from Patent WO0146417. AX179789 ttaaaatctcaaaaaa 741 726 ΩĐ ò Ŋ

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1 (sites), Volughtus,M., Carter,K.C., Ebner,R., Endress,G., Horrigan,S., Soppet,D.R. and Weaver,Z. Cancer gene determination and therapeutic screening using signature
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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49.6%; Score 377.2; DB 6;
Best Local Similarity 99.2%; Pred. No. 3.2e-75;
Matches 379; Conservative 0; Mismatches 3;
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Avalon Pharmaceuticals (US)
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                                                                   Sequence 5510 from Patent W00194629.
AX335001
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Sequence 7 from Patent WO0146417.
AX179787
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota: Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 603)

Walke, D.W. and Turner, C.A.

Human membrane proteins and polynucleotides encoding the same having homology to cd20 proteins and ige receptors

Patent: Wo 0146417-A 1 28-JUN-2001;

Lexicon Genetics Incorporated (US)

Location/Qualifiers
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Pred. No. 4e-125;
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                                                         Sequence 1 from Patent W00146417.
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Best Local Similarity 99.5%;
Matches 600; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (2005) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 1 (400) 
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Walke, D.W. and Turner, C.A. Human membrane proteins and polynucleotides encoding the same having homology to cd20 proteins and ige receptors patent; WO 0146417A. 5 28-UNN-2001; Lexicon Genetics Incorporated (US)
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/db_xref="taxon:9606"
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Anderson, S., Baldwin, J., Barna, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Bouskhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Grahan, L., Grant, G., Canto, M., Erreita, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graha, H., Grant, G., Landson, R., Heaford, A., Horton, L., Klein, J., Larocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McBwan, P., McGurk, A., McKernan, K., McPheeters, R., McGurk, A., McKernan, K., McPheeters, R., McGurk, A., McKernan, C., H., O'Connor, T., O'Connell, P., O'Neil, D., Ollvar, T., Norman, C.H., O'Connor, T., O'Donnell, P., Psani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Tralamas, J., Vossillev, H., Vola, R., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zahnoun, J., Zimmer, A. and Zody, M., Travers, M., Trigillo, J., Voung, G., Zahnoun, J., Zimmer, A. and Zody, M., Submitted (01-App. 2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 18, 2000 this sequence version replaced g1:7382629.
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Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 138097)
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                                                                                                                                                                                                                                                                           158 tcagaatatgagtccacagaactttcagccacgaccttttcaactccaaagccccttgcaa 217
                                                                                                                                                                                                                                                                                                                                                                                               218 aaattatttgctagaaaaatgaaaatcttagggactatccagatcctgtttggaattatg 277
                                                                                                                                                                                 ACULITBY 138097 bp DNA linear HTG 18-AUK HOMO Sapiens chromosome 15 clone RP11-196E16 map 15, LOW-PASS SEQUENCE SAMPLING.
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                                Length 417;
Score 340.2; DB 6; Leus...
Pred. No. 7.3e-67;
--t-nhos 3; Indels
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                                                                                      0; Mismatches
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                         44.8%;
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in length

in length

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93 37992: gap of 100 bp 3872: contig of 680 bp in length 33 8772: contig of 680 bp in length 73 39475: contig of 703 bp in length 76 39575: gap of 100 bp 640290: contig of 715 bp in length 91 43990: gap of 697 bp in length 91 41087: contig of 697 bp in length
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36308: contig of 725 bp in length
36408: gap of 100 bp
37108: contig of 700 bp in length
37208: gap of 100 bp
37892: contig of 684 bp in length
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45189 45880: contig of 692 bp in length
45881 45980: gap of 100 bp
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46884 46783: gap of 100 bp
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33951: contig of 694 bp in length
34521: gap of 100 bp
34735: contig of 684 bp in length
34835: gap of 100 bp
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45088; contig of 693 bp in length
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3356: contig of 695 bp in length
60: gap of 100 bp
3157: contig of 697 bp in length
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30084 30775; contig of 692 bp in length
30775 30875; gap of 100 bp
30876 31565; contig of 690 bp in length
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35483: contig of 648 bp in length
                   37 21233: contig of 697 bp in 34 21333: gap of 100 bp 13 22142: gap of 100 bp 13 22142: gap of 100 bp 13 22808: contig of 666 bp in 3 22808: contig of 666 bp in 3 2395: contig of 687 bp in 3 2395: gap of 100 bp 13 2491: gap of 100 bp 13 2491: gap of 100 bp 13 25190: contig of 699 bp in 32 25190: contig of 699 bp in 3 25190: contig of
20536: gap of 10
21233: contig of 0
21333: gap of 10
22042: contig of 0
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                                                                            Center: Whitehead Institute/ MIT Center for Genome Research Center code: Wilhtehead Institute/ MIT Center for Genome Research Center code: Wilkw-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project name: 19008
Center project name: 196_E_16
                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This record contains 163 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* Will be sequenced to completion. In the event that
* the record is updated, the accession number will
       Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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1 5523: gap of 100
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1 (bases 1 to 138097)

Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo saplens chromosome 15, clone RP11-196E16

2 (bases 1 to 138097)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109559 CTABARTCATCTCTTTCABARTATCACCGACACCATCATGAGGATTCAAGCACCGCACACAG 109618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DD 109619 TCCGGTGTTTCTGGTATTTCCTCCAGAAATCACTGCTTCAGAATATGAGTCCACAGAACT 109678
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                                                                                                                                                                                                                                                                                                                                                              Score 250.4; DB 2; Length 138097;
Pred. No. 1.2e-46;
0; Mismatches 6; Indels 0; 0
                                                                       50784: gap of 100 bp 51507: contig of 723 bp in length 51607: gap of 100 bp 52420: gap of 100 bp 100 bp 100 bp 100 bp 53133: contig of 713 bp in length 5343: contig of 713 bp in length 5353: contig of 713 bp in length
49979: contig of 702 bp in length
49979: gap of
50684: contig of 705 bp in length
                                                                                                                                                                                                                                   53233: gap of 100 bp 53933: contig of 700 bp in length
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Best Local Similarity 97.7%;
Matches 254; Conservative (
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AUTHORS
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Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigillo,J.,
Vasailiev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
                                                                                                                   for Genome
                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                             Submitted (01.APR-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA on Aug 18, 2000 this sequence version replaced gi:7382629. All repeats were identified using RepeatMasker: Smit, A.F. A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
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of 701 bp in length
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f 711 bp
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of 695 bp :
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Center clone name: 196_E_16
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1564: gap of
2268: contig of
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12582:
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3042: con
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7837: con:
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13490 14186: con
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5423: con
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3820: con
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4626; cor
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7040: cor
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18684 174776; contig of 683 bp in length 18777 1478 1879 off of 1702 bp in length 18779 1878; contig of 684 bp in length 18779 1878; contig of 684 bp in length 18779 1878; contig of 681 bp in length 18774 20256; gap of 681 bp in length 19774 20256; gap of 681 bp in length 19774 20256; gap of 681 bp in length 18774 20256; gap of 100 bp 18774 20256; gap of 100 bp 18775 18

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pirren, B., Linton, L., Nusbaum, C. and Lander, E.
Burren, B., Linton, L., Nusbaum, C. and Lander, E.
Burren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baldwin, J., Barna, N., Beckerly, R., Boyuslawkiy, L., Boukhgalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gaqe, D.,
Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,
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Homo sapiens clone RP11-24D1, WORKING DRAFT SEQUENCE, 5 unordered
pieces.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 147788)
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Pred. No. 1.2e-46;
0; Mismatches 6; Indels 0;
    45881 45980: gap of 100 bp 45981 46683: contig of 703 bp in length 46684 47481: contig of 698 bp in length 47482 47481: contig of 698 bp in length 47482 47581: gap of 100 bp 47582 48290: contig of 709 bp in length 48291 48390: gap of 100 bp 49881 49977: contig of 709 bp in length 49080 4979: gap of 100 bp 50685 50785 51807: contig of 702 bp in length 50784: gap of 508 bp in length 50785 51807: contig of 703 bp in length 50785 51807: contig of 703 bp in length 50785 51807: contig of 703 bp in length 50785 51807: contig of 713 bp in length 51308 51313: contig of 713 bp in length 51313: contig of 713 bp in length 51313: gap of 100 bp 51313: gap of 5100 bp in length 53234 5333: gap of 100 bp in length 53234 5333: gap of 100 bp in length 53334 54333: gap of 100 bp in length 54034 54703: contig of 670 bp in length
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AC015840.2 GI:7657730
HTG; HTGS_PHASE1; HTGS_DRAFT.
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97.7%;
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Best Local
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KEYWORDS
SOURCE
ORGANISM
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TITLE
JOURNAL
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McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morracwi, J., Norman, C.H., O'Conner, T., O'Connell, P., Peterson, K., Paylor, J., Norman, C.H., O'Conner, T., O'Connell, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Testafaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

L. Submission

L. Submitsed (J.Nov. 1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 27, 2000 this sequence version replaced gi:6446828.

All repeals were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ...... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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Sequencing vector: M13, M77815; 10% of reads Chemistry: Dye-terminator B1g Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 136347 bases at least 030 consensus quality: 143600 bases at least 030 consensus quality: 14612 bases at least 030 insert size: 203000; agarose-fp Insert size: 203000; agarose-fp Insert size: 147388; sum-of-contigs Quality coverage: 5.2 in 020 bases; sum-of-contigs Quality coverage: 7.1 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16188 16287; gap of 100 bp 16288 25089; contig of 8802 bp in length 25090 25189; gap of 100 bp 25190 63923; contig of 38734 bp in length 64024 147788; contig of 83765 bp in length. Location/Qualifiers
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/clone_lib="RPCI-11 Human Male
L. .6594
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6695. .16187
1628. .25089
/note="assembly_fragment"
16288. .25089
/note="assembly_fragment clone_end:SP6
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/db_xref="taxon:9606"
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Homo sapiens genomic DNA, chromosome 11q clone:RP11-710G6, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 128070 TCCGGTGTTTCTGGTATTTCCTCCAGAAATCACTGCTTCAGAATATGAGTCCACAGAACT 128129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                  121 tccggtgtttctggtatttcctccagaaatcactgcttcagaatatgagtccacagaact 180
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                                                                                                                                             1 ttccaqtqctccaggcagcctcagcacaagaaaaagaacatggtctagactgaagtaccaa 60
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Length 147788;
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                                                                          Indels
   32.9%; Score 250.4; DB 2;
llarity 97.7%; Pred. No. 1.2e-46;
Conservative 0; Mismatches 6;
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Pred. No. 1.1e-46;
0; Mismatches 6;
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50087 a 31927 c 31564 g 47660 t
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Best Local Similarity 97.7%;
Matches 254; Conservative
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                                        Similarity
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                                        Best Local Sim
Matches 254;
   Query Match
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 167934)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Matanabe,H. and Sakaki,Y.

Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Submitted (06-JAN-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suebhro-Chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mall:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9117)

Tel:81-45-503-9111, Fax:81-45-503-9170)

On Nov 5, 2001 this sequence version replaced gi:11176992.
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Homo sapiens genomic DNA, chromosome 11q clone:RP11-72984, complete
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the accession number will be preserved.
1 166793: contig of 166793 bp in length.
Location/Qualiflers
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                                                                                                                                                                                                                                                                                         /clone_lib="RPCI-11 Human Male BAC"
31834 c 32914 g 55586 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 250.4; DB 2;
Pred. No. 1.1e-46;
0; Mismatches 6;
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Homo sapiens
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                                                                                             1. .166793
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome≈"11"
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Best Local Similarity 97.7%;
Matches 254; Conservative
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Barren, B. Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barren, W., Bastlen, Y., Choepel, Y., Colangelo, M., Collins, S., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farco, S., Ferreira, P., FitzHuph, W., Gade, D., Galagan, J., Gardyna, S., Glode, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, K., Landers, T., Lehoczky, J., Levine, R., Lind, G., MacCean, C., Macdonald, P., Marthews, C., McCarthy, M., McDew, C., Norman, C. H., Marthews, C., McCarthy, M., McDew, C., Norman, C. H., Murphy, T., Naylor, J., Meney, C., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Nell, D., Oliver, J., Peterson, R., Ried, K., Rise, C., Ragov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Strauss, N., Subramanian, A., Talanas, J., Tesfave, S., Theodore, J., Travers, M., Travis, M., Trigilio, J., Voung, G., Zainoun, J., Zembok, L., Zimmer, A. and Zody, M., Zembok, L., Zimmer, A. and Zody, M., Santos, A. and Zody, M., Santos, A. and Zody, M., Zembok, L., Zimmer, A. and Zody, M
                                                                                                                                                                                                                                                                                                                                                                                                           AC090401 166793 bp DNA linear HTG 14-OCT-2001 Homo sapiens chromosome 11 clone RP11-729B4 map 11, *** SEQUENCING IN PROGRESS ***, I ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON Sep 20, 2001 this sequence version replaced gi:14971278.

All repeats were identified using RepeatMasKer:
Smit, A.F.A. 6 Green, P. (1996-1997)

Http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 166793) Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 11, clone RP11-72984
Db 133619 TCCGGTGTTTCTGGTATTTCCTCCAGAAATCACTTCAGAATATGAGTCCACAGAACT 133678
                                                                                             Db 133679 TTCAGCCACGACCACTTTCAACTCAAAGCCCCTTGCAAAAATTATTTGCTAGAAAAATGAA 133738
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Center: Whitehead Institute/ MIT Center for Genome Research
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* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
                                                                 ttcagccacgaccttttcaactcaaagccccttgcaaaaattatttgctagaaaatgaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
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ŒΣ	est Lo	cal Sim 254;	Best Local Similarity 97.7 Matches 254; Conservative	97.78 vative	a :	red.	Best Local Similarity 97.7%; Pred. No. 1.1e-46; Matches 254; Conservative 0; Mismatches 6	; 6;	.46; 6; Indels	0;	Gaps		0;	
ð	1	ttccag	rgctcca	ggcagcct	cago	acaa	ttocagtgctccaggcacctcagcacaaggaacatggtctagactgaagtaccaa	ggtct	agactgaag	tacca	1a 60			
Q	22624	TTCCAG	TGCTCCA	GGCAGCCT	CAGC	ACA	TICCAGTGCTCCAGGCGCCTCAGCACAAGAAAAAAAGACATGGTCTAGACTGAAGTACCAA 22683	GGTCT	AGACTGAAG	TACC	A 226	583		
ď	61	ctaaat	catetee	tttcaaat	tato	accg	61 ctaaatcatctcctttcaaattatcaccgacaccatcatggattcaagcaccgcacacg 120	gatto	aagcaccac	acace	1g 120			
g	22684		CATCTCC	TTTCAAAT	TATC	ACCG	CIAAATCATCTCCTTTCAAATTATCACCGACACCATCATGGATTCAAGGACTCGCCCACAG 22743	GATTC	AAGCACCGC	ACACA	NG 227	743		
δ	121	tccggt	gtttctg	gtatttcc	tcca	gaaa	121 tocggtgtttctggtatttctctcagaaatcactgcttcagaatatgagtccacagaact 180	gaata	tgagtccac	sagaad	st 180	0		
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ý	181	ttcagc	cacgacc	tttcaac	tcaa	agcc	ttcagccacgaccttttcaactcaaagcccttgcaaaaattatttgctagaaaatgaa 240	ttatt	tgctagaaa	aatga	1a 24(0		
a	22804		CACGACC	TTTCAAC	TCAA	AGCC	TTCAGCCACGACCTTTTCAACTCAAAGCCCCTTGCAAAAATTTTGCTAGAAAATGAA 22863	TTATT	TGCTAGAA	AAATG2	VA 228	863		
ò	241	aatctt	agggact	241 aatettagggaetateeaga 260	260									
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Search completed: August 30, 2002, 02:46:47 Job time: 7480 sec

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/organism="Homo sapiens"/db_xref="GDB:5927437"
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                                                                                                                                                                                                                                                                                                                                                                                                           /sex="male"
/lab_host="DH10B"
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Best Local Similarity 99.6%;
Matches 506; Conservative (
    Eutheria;
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0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NHMGC Library." 1 others
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                             121 TGGTATTTCCTCCAGAAATCACTGCTTCAGAATATGAGTCCACAGAACTTTCAGCCACGA 180
                                                                                                                                                                                                                                                                                                                                                                             251
                                                                                                                                                                                                                                                                                                                                                                                                      181 CCTTTTCAACTCAAAGCCCCCTTGCAAAATTATTTGCTAGAAAATGAAAATCTTAGGGA 240
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                                                                                                                                                         Gaps
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                                                                                                                         Length 713;
                                                                                                                                                         4; Indels
                                                                                                                        DB 10;
                                                                                                                        Score 707.2; DB 10
Pred. No. 9.7e-90;
0; Mismatches 4;
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AA436088
AA436088.1 GI:2141002
                                                                                                                         Query Match 93.1%;
Best Local Similarity 99.4%;
Matches 709; Conservative
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Primates; Catarrhini; Hominidae; Homo
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Pred. No. 1.7e-61;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:730742"
/clone_lib="Soares_testis_NHT"
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 74 Std Error: 0.00
Seq primer: -40ml3 wd. Er from Amersham
High quality sequence stop: 455.
High quality contain/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ogapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
                                                                                                                                                                                    AII49899 508 bp mRNA linear EST 10-NOV-1998 qf43h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752827 3' similar to SW:CD20_HUMAN P11836 B-LYMPHOCYTE ANTIGEN CD20 ;,
                                                                                                                                                                                                                                                                                                                  Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 508)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
8 NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 ggagttatcttccttttcactttgttaaaaccatatccaaggtttccctttatatttctt 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1467 agtgccctgggagcaatagctggaatcattctcctcacatttggtttcatcctagatcaa 526
                       421 AGTGCCCTGGGACCAATAGCTGGAATCATTCTCCTCACATTTGGTTTCATCCTAGATCAA 480
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Pred. No. 2.9e-61;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:1752827"
/clone_11b="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                           AI149899.1 GI:3678368
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                                                                                                                                                                                                                                       mRNA sequence.
AI149899
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; ist strand cDNA was prepared from mNRA obtained from Clontech Laboratories inc., and primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aA416972 1997 2194h05.81 Soares_testis_NHT Homo sapiens CDNA clone IMAGE:730041 3' similar to SW:CD20_HUMAN P11836 B-LYMPHOCYTE ANTIGEN CD20 ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wyle,T., Waterston,R. and Wilson,R.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 387)
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@tmage.llnl.gov) for further information.
Insert Length: 656 Error: 0.00
Seq primer: -41ml3 fwd. ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                          649
                                                                                                                                                                                                                         209
                     gtgaaaagaaaaaocacagaaactctgataatattgagccgaataatgaattttcttagt 469
tcaggatatccattctggggctctgttttgttcattaattctggagccttcctaattgca 409
                                                                                                                                 328 GTGAAAAGAAAAACCCACAGAAACTCTGATAATATTGAGCCGAATAATGAATTTTCTTAGT 269
                                                                                                                                                                                                                                                                                                                                                                                                       88
                                                                                                                                                                              530 tacatttgtggttattctcaccaaaatagtcagtgtaaggctgttactgtcctgttcttg
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                                                                                                                                                                                                                                                                                                                                                                                    Confect: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 17e1: 314 286 1800
Fax: 314 286 1810
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/db_xref="taxon:9606"
/clone="IMAGE:730041"
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